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(54) Title: NANBV DIAGNOSTICS AND VACCINES

(57) Abstract

A family of cDNA sequences derived from hepatitis C virus (HCV) are provided. These sequences encode antigens which react immunologically with antibodies present in individuals with non-A non-B hepatitis (NANBH), but which generally are absent from individuals infected with hepatitis A virus (HAV) or hepatitis B virus (HBV), and also are absent from control individuals. A comparison of these cDNA sequences with the sequences in Genebank, and with the sequences of hepatitis delta virus (HDV) and HBV shows a lack of substantial homology. A comparison of the sequences of amino acids encoded in the cDNA with the sequences of Flaviviruses indicates that HCV is a Flavivirus or Flavi-like virus. The HCV cDNA sequences are useful for the design of polynucleotide probes, and for the synthesis of polypeptides which may be used in immunoassays. Both the polynucleotide probes and the polypeptides may be useful for the diagnosis of HCV-induced NANBH, and for screening blood bank specimens and donors for HCV infection. In addition, these cDNA sequences may be useful for the synthesis of immunogenic polypeptides which may be used in vaccines for the treatment, prophylactic and/or therapeutic, of HCV infection. Polypeptides encoded within the cDNA sequences may also be used to raise antibodies against HCV antigens, and for the purification of antibodies directed against HCV antigens. These antibodies may be useful in immunoassays for detecting HCV antigens associated with NANBH in individuals, and in blood bank donations. Moreover, these antibodies may be used for treatment of NANBH in individuals. The reagents provided in the invention also enable the isolation of NANBH agent(s), and the propagation of these agent(s) in tissue culture systems. Moreover, they provide reagents which are useful for screening for antiviral agents for HCV, particularly in tissue culture or animal model systems.

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-1-

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NANBV DIAGNOSTICS AND VACCINES

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Technical Field

The invention relates to materials and methodologies for managing the spread of non-A, non-B hepatitis virus (NANBV) infection. More specifically, it relates to diagnostic DNA fragments, diagnostic proteins, diagnostic antibodies and protective antigens and antibodies for an etiologic agent of NANB hepatitis, i.e., hepatitis C virus.

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U.S. Patent No. 4,472,500  
U.S. Patent No. 4,491,632  
U.S. Patent No. 4,493,890

15 Background Art

Non-A, Non-B hepatitis (NANBH) is a transmissible disease or family of diseases that are believed to be viral-induced, and that are distinguishable from other forms of viral-associated liver diseases, including that caused by the known hepatitis viruses, i.e., hepatitis A virus (HAV), hepatitis B virus (HBV), and delta hepatitis virus (HDV), as well as the hepatitis induced by cytomegalovirus (CMV) or Epstein-Barr virus (EBV). NANBH was first identified in transfused individuals. Transmission from man to chimpanzee and serial passage in chimpanzees provided evidence that NANBH is due to a transmissible infectious agent or agents. However, the transmissible agent responsible for NANBH is still unidentified and the number of agents which are causative of the disease are unknown.

Epidemiologic evidence is suggestive that there may be three types of NANBH: the water-borne epidemic type; the blood or needle associated type; and the sporadically occurring (community acquired) type.

-6-

However, the number of agents which may be the causative of NANBH are unknown.

Clinical diagnosis and identification of NANBH has been accomplished primarily by exclusion of other 5 viral markers. Among the methods used to detect putative NANBV antigens and antibodies are agar-gel diffusion, counterimmunoelectrophoresis, immunofluorescence microscopy, immune electron microscopy, radioimmunoassay, and enzyme-linked immunosorbent assay. However, none of 10 these assays has proved to be sufficiently sensitive, specific, and reproducible to be used as a diagnostic test for NANBH.

Until now there has been neither clarity nor agreement as to the identity or specificity of the antigen 15 antibody systems associated with agents of NANBH. This is due, at least in part, to the prior or co-infection of HBV with NANBV in individuals, and to the known complexity of the soluble and particulate antigens associated with HBV, as well as to the integration of HBV DNA into the genome 20 of liver cells. In addition, there is the possibility that NANBH is caused by more than one infectious agent, as well as the possibility that NANBH has been misdiagnosed. Moreover, it is unclear what the serological assays detect 25 in the serum of patients with NANBH. It has been postulated that the agar-gel diffusion and counterimmuno- electrophoresis assays detect autoimmune responses or non-specific protein interactions that sometimes occur between serum specimens, and that they do not represent specific 30 NANBV antigen-antibody reactions. The immunofluorescence, and enzyme-linked immunosorbent, and radioimmunoassays appear to detect low levels of a rheumatoid-factor-like material that is frequently present in the serum of patients with NANBH as well as in patients with other hepatic and nonhepatic diseases. Some of the reactivity

detected may represent antibody to host-determined cytoplasmic antigens.

There are a number of candidate NANBV. See, for example the reviews by Prince (1983), Feinstone and 5 Hoofnagle (1984), and Overby (1985, 1986, 1987) and the article by Iwarson (1987). However, there is no proof that any of these candidates represent the etiological agent of NANBH.

The demand for sensitive, specific methods for 10 screening and identifying carriers of NANBV and NANBV contaminated blood or blood products is significant. Post-transfusion hepatitis (PTH) occurs in approximately 10% of transfused patients, and NANBH accounts for up to 15 90% of these cases. The major problem in this disease is the frequent progression to chronic liver damage (25-55%).

Patient care as well as the prevention of transmission of NANBH by blood and blood products or by close personal contact require reliable diagnostic and prognostic tools to detect nucleic acids, antigens and 20 antibodies related to NANBV. In addition, there is also a need for effective vaccines and immunotherapeutic therapeutic agents for the prevention and/or treatment of the disease.

25 Disclosure of the Invention

The invention pertains to the isolation and characterization of a newly discovered etiologic agent of NANBH, hepatitis C virus (HCV). More specifically, the invention provides a family of cDNA replicas of portions 30 of HCV genome. These cDNA replicas were isolated by a technique which included a novel step of screening expression products from cDNA libraries created from a particulate agent in infected tissue with sera from patients with NANBH to detect newly synthesized antigens 35 derived from the genome of the heretofore unisolated and

uncharacterized viral agent, and of selecting clones which produced products which reacted immunologically only with sera from infected individuals as compared to non-infected individuals.

5       Studies of the nature of the genome of the HCV, utilizing probes derived from the HCV cDNA, as well as sequence information contained within the HCV cDNA, are suggestive that HCV is a Flavivirus or a Flavi-like virus.

10      Portions of the cDNA sequences derived from HCV are useful as probes to diagnose the presence of virus in samples, and to isolate naturally occurring variants of the virus. These cDNAs also make available polypeptide sequences of HCV antigens encoded within the HCV genome(s) and permits the production of polypeptides which are useful as standards or reagents in diagnostic tests and/or as components of vaccines. Antibodies, both polyclonal and monoclonal, directed against HCV epitopes contained within these polypeptide sequences are also useful for diagnostic tests, as therapeutic agents, for screening of 15 antiviral agents, and for the isolation of the NANBV agent from which these cDNAs derive. In addition, by utilizing probes derived from these cDNAs it is possible to isolate and sequence other portions of the HCV genome, thus giving rise to additional probes and polypeptides which are useful in the diagnosis and/or treatment, both prophylactic and therapeutic, of NANBH.

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Accordingly with respect to polynucleotides, some aspects of the invention are: a purified HCV polynucleotide; a recombinant HCV polynucleotide; a recombinant polynucleotide comprising a sequence derived from an HCV genome or from HCV cDNA; a recombinant polynucleotide encoding an epitope of HCV; a recombinant vector containing any of the above recombinant polynucleotides, and a host cell transformed with any of 30 these vectors.

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Other aspects of the invention are: a recombinant expression system comprising an open reading frame (ORF) of DNA derived from an HCV genome or from HCV cDNA, wherein the ORF is operably linked to a control sequence compatible with a desired host, a cell transformed with the recombinant expression system, and a polypeptide produced by the transformed cell.

Still other aspects of the invention are: purified HCV, a preparation of polypeptides from the purified HCV; a purified HCV polypeptide; a purified polypeptide comprising an epitope which is immunologically identifiable with an epitope contained in HCV.

Included aspects of the invention are a recombinant HCV polypeptide; a recombinant polypeptide comprised of a sequence derived from an HCV genome or from HCV cDNA; a recombinant polypeptide comprised of an HCV epitope; and a fusion polypeptide comprised of an HCV polypeptide.

Also included in the invention are a monoclonal antibody directed against an HCV epitope; and a purified preparation of polyclonal antibodies directed against an HCV epitope.

Another aspect of the invention is a particle which is immunogenic against HCV infection comprising a non-HCV polypeptide having an amino acid sequence capable of forming a particle when said sequence is produced in a eukaryotic host, and an HCV epitope.

Still another aspect of the invention is a polynucleotide probe for HCV.

Aspects of the invention which pertain to kits are those for: analyzing samples for the presence of polynucleotides derived from HCV comprising a polynucleotide probe containing a nucleotide sequence from HCV of about 8 or more nucleotides, in a suitable container; analyzing samples for the presence of an HCV

-10-

antigen comprising an antibody directed against the HCV antigen to be detected, in a suitable container; analyzing samples for the presence of an antibodies directed against an HCV antigen comprising a polypeptide containing an HCV epitope present in the HCV antigen, in a suitable container.

Other aspects of the invention are: a polypeptide comprised of an HCV epitope, attached to a solid substrate; and an antibody to an HCV epitope, attached to a solid substrate.

Still other aspects of the invention are: a method for producing a polypeptide containing an HCV epitope comprising incubating host cells transformed with an expression vector containing a sequence encoding a polypeptide containing an HCV epitope under conditions which allow expression of said polypeptide; and a polypeptide containing an HCV epitope produced by this method.

The invention also includes a method for detecting HCV nucleic acids in a sample comprising reacting nucleic acids of the sample with a probe for an HCV polynucleotide under conditions which allow the formation of a polynucleotide duplex between the probe and the HCV nucleic acid from the sample; and detecting a polynucleotide duplex which contains the probe.

Immunoassays are also included in the invention. These include an immunoassay for detecting an HCV antigen comprising incubating a sample suspected of containing an HCV antigen with a probe antibody directed against the HCV antigen to be detected under conditions which allow the formation of an antigen-antibody complex; and detecting an antigen-antibody complex containing the probe antibody. An immunoassay for detecting antibodies directed against an HCV antigen comprising incubating a sample suspected of containing anti-HCV antibodies with a probe polypeptide

which contains an epitope of the HCV, under conditions which allow the formation of an antibody-antigen complex; and detecting the antibody-antigen complex containing the probe antigen.

5           Also included in the invention are vaccines for treatment of HCV infection comprising an immunogenic peptide containing an HCV epitope, or an inactivated preparation of HCV, or an attenuated preparation of HCV.

10          Another aspect of the invention is a tissue culture grown cell infected with HCV.

15          Yet another aspect of the invention is a method for producing antibodies to HCV comprising administering to an individual an isolated immunogenic polypeptide containing an HCV epitope in an amount sufficient to produce an immune response.

20          Still another aspect of the invention is a method for isolating cDNA derived from the genome of an unidentified infectious agent, comprising: (a) providing host cells transformed with expression vectors containing a cDNA library prepared from nucleic acids isolated from tissue infected with the agent and growing said host cells under conditions which allow expression of polypeptide(s) encoded in the cDNA; (b) interacting the expression products of the cDNA with an antibody containing body component of an individual infected with said infectious agent under conditions which allow an immunoreaction, and detecting antibody-antigen complexes formed as a result of the interacting; (c) growing host cells which express polypeptides that form antibody-antigen complexes in step 25 (b) under conditions which allow their growth as individual clones and isolating said clones; (d) growing cells from the clones of (c) under conditions which allow expression of polypeptide(s) encoded within the cDNA, and interacting the expression products with antibody containing body components of individuals other than the

-12-

individual in step (a) who are infected with the infectious agent and with control individuals uninfected with the agent, and detecting antibody-antigen complexes formed as a result of the interacting; (e) growing host 5 cells which express polypeptides that form antibody- antigen complexes with antibody containing body components of infected individuals and individuals suspected of being infected, and not with said components of control individuals, under conditions which allow their growth as 10 individual clones and isolating said clones; and (f) isolating the cDNA from the host cell clones of (e).

Brief Description of the Drawings

Fig. 1 shows the double-stranded nucleotide sequence of the HCV cDNA insert in clone 5-1-1, and the putative amino acid sequence of the polypeptide encoded therein.

Fig. 2 shows the homologies of the overlapping HCV cDNA sequences in clones 5-1-1, 81, 1-2, and 91.

Fig. 3 shows a composite sequence of HCV cDNA derived from overlapping clones 81, 1-2, and 91, and the amino acid sequence encoded therein.

Fig. 4 shows the double-stranded nucleotide sequence of the HCV cDNA insert in clone 81, and the putative amino acid sequence of the polypeptide encoded therein.

Fig. 5 shows the HCV cDNA sequence in clone 36, the segment which overlaps the NANBV cDNA of clone 81, and the polypeptide sequence encoded within clone 36.

Fig. 6 shows the combined ORF of HCV cDNAs in clones 36 and 81, and the polypeptide encoded therein.

Fig. 7 shows the HCV cDNA sequence in clone 32, the segment which overlaps clone 81, and the polypeptide encoded therein.

-13-

Fig. 8 shows the HCV cDNA sequence in clone 35, the segment which overlaps clone 36, and the polypeptide encoded therein.

5 Fig. 9 shows the combined ORF of HCV cDNAs in clones 35, 36, 81, and 32, and the polypeptide encoded therein.

Fig. 10 shows the HCV cDNA sequence in clone 37b, the segment which overlaps clone 35, and the polypeptide encoded therein.

10 Fig. 11 shows the HCV cDNA sequence in clone 33b, the segment which overlaps clone 32, and the polypeptide encoded therein.

15 Fig. 12 shows the HCV cDNA sequence in clone 40b, the segment which overlaps clone 37b, and the polypeptide encoded therein.

Fig. 13 shows the HCV cDNA sequence in clone 25c, the segment which overlaps clone 33b, and the polypeptide encoded therein.

20 Fig. 14 shows the nucleotide sequence and polypeptide encoded therein of the ORF which extends through the HCV cDNAs in clones 40b, 37b, 35, 36, 81, 32, 33b, and 25c.

25 Fig. 15 shows the HCV cDNA sequence in clone 33c, the segment which overlaps clones 40b and 33c, and the amino acids encoded therein.

Fig. 16 shows the HCV cDNA sequence in clone 8h, the segment which overlaps clone 33c, and the amino acids encoded therein.

30 Fig. 17 shows the HCV cDNA sequence in clone 7e, the segment which overlaps clone 8h, and the amino acids encoded therein.

Fig. 18 shows the HCV cDNA sequence in clone 14c, the segment which overlaps clone 25c, and the amino acids encoded therein.

-14-

Fig. 19 shows the HCV cDNA sequence in clone 8f, the segment which overlaps clone 14c, and the amino acids encoded therein.

5 Fig. 20 shows the HCV cDNA sequence in clone 33f, the segment which overlaps clone 8f, and the amino acids encoded therein.

10 Fig. 21 shows the HCV cDNA sequence in clone 33g, the segment which overlaps clone 33f, and the amino acids encoded therein.

15 Fig. 22 shows the HCV cDNA sequence in clone 7f, the segment which overlaps the sequence in clone 7e, and the amino acids encoded therein.

Fig. 23 shows the HCV cDNA sequence in clone 11b, the segment which overlaps the sequence in clone 7f, and the amino acids encoded therein.

15 Fig. 24 shows the HCV cDNA sequence in clone 14i, the segment which overlaps the sequence in clone 11b, and the amino acids encoded therein.

20 Fig. 25 shows the HCV cDNA sequence in clone 39c, the segment which overlaps the sequence in clone 33g, and the amino acids encoded therein.

25 Fig. 26 shows a composite HCV cDNA sequence derived from the aligned cDNAs in clones 14i, 11b, 7f, 7e, 8h, 33c 40b 37b 35 36, 81, 32, 33b, 25c, 14c, 8f, 33f, and 33g; also shown is the amino acid sequence of the polypeptide encoded in the extended ORF in the derived sequence.

30 Fig. 27 shows the sequence of the HCV cDNA in clone 12f, the segment which overlaps clone 14i, and the amino acids encoded therein.

Fig. 28 shows the sequence of the HCV cDNA in clone 35f, the segment which overlaps clone 39c, and the amino acids encoded therein.

-15-

Fig. 29 shows the sequence of the HCV cDNA in clone 19g, the segment which overlaps clone 35f, and the amino acids encoded therein.

5 Fig. 30 shows the sequence of clone 26g, the segment which overlaps clone 19g, and the amino acids encoded therein.

Fig. 31 shows the sequence of clone 15e, the segment which overlaps clone 26g, and the amino acids encoded therein.

10 Fig. 32 shows the sequence in a composite cDNA, which was derived by aligning clones 12f through 15e in the 5' to 3' direction; it also shows the amino acids encoded in the continuous ORF.

15 Fig. 33 shows a photograph of Western blots of a fusion protein, SOD-NANB<sub>5-1-1</sub>, with chimpanzee serum from chimpanzees infected with BB-NANB, HAV, and HBV.

Fig. 34 shows a photograph of Western blots of a fusion protein, SOD-NANB<sub>5-1-1</sub>, with serum from humans infected with NANBV, HAV, HBV, and from control humans..

20 Fig. 35 is a map showing the significant features of the vector pAB24.

Fig. 36 shows the putative amino acid sequence of the carboxy-terminus of the fusion polypeptide C100-3 and the nucleotide sequence encoding it.

25 Fig. 37A is a photograph of a coomassie blue stained polyacrylamide gel which identifies C100-3 expressed in yeast.

Fig. 37B shows a Western blot of C100-3 with serum from a NANBV infected human.

30 Fig. 38 shows an autoradiograph of a Northern blot of RNA isolated from the liver of a BB-NANBV infected chimpanzee, probed with BB-NANBV cDNA of clone 81.

Fig. 39 shows an autoradiograph of NANBV nucleic acid treated with RNase A or DNase I, and probed with BB-35 NANBV cDNA of clone 81.

-16-

Fig. 40 shows an autoradiograph of nucleic acids extracted from NANBV particles captured from infected plasma with anti-NANB<sub>5-1-1</sub>, and probed with <sup>32</sup>P-labeled NANBV cDNA from clone 81.

5 Fig. 41 shows autoradiographs of filters containing isolated NANBV nucleic acids, probed with <sup>32</sup>P-labeled plus and minus strand DNA probes derived from NANBV cDNA in clone 81.

10 Fig. 42 shows the homologies between a polypeptide encoded in HCV cDNA and an NS protein from Dengue flavivirus.

Fig. 43 shows a histogram of the distribution of HCV infection in random samples, as determined by an ELISA screening.

15 Fig. 44 shows a histogram of the distribution of HCV infection in random samples using two configurations of immunoglobulin-enzyme conjugate in an ELISA assay.

Fig. 45 shows the sequences in a primer mix, derived from a conserved sequence in NS1 of flaviviruses.

20 Fig. 46 shows the HCV cDNA sequence in clone k9-1, the segment which overlaps the cDNA in Fig. 26, and the amino acids encoded therein.

Fig. 47 shows the sequence in a composite cDNA which was derived by aligning clones k9-1 through 15e in 25 the 5' to 3' direction; it also shows the amino acids encoded in the continuous ORF.

#### Modes for Carrying Out the Invention

##### 30 I. Definitions

The term "hepatitis C virus" has been reserved by workers in the field for an heretofore unknown etiologic agent of NANBH. Accordingly, as used herein, "hepatitis C virus" (HCV) refers to an agent causitive of 35 NANBH, which was formerly referred to as NANBV and/or BB-

NANBV. The terms HCV, NANBV, and BB-NANBV are used interchangeably herein. As an extension of this terminology, the disease caused by HCV, formerly called NANB hepatitis (NANBH), is called hepatitis C. The terms NANBH and 5 hepatitis C may be used interchangeably herein.

The term "HCV", as used herein, denotes a viral species which causes NANBH, and attenuated strains or defective interfering particles derived therefrom. As shown infra., the HCV genome is comprised of RNA. It is 10 known that RNA containing viruses have relatively high rates of spontaneous mutation, i.e., reportedly on the order of  $10^{-3}$  to  $10^{-4}$  per nucleotide (Fields & Knipe (1986)). Therefore, there are multiple strains within the HCV species described infra. The compositions and methods 15 described herein, enable the propagation, identification, detection, and isolation of the various related strains. Moreover, they also allow the preparation of diagnostics and vaccines for the various strains, and have utility in screening procedures for anti-viral agents for 20 pharmacologic use in that they inhibit replication of HCV.

The information provided herein, although derived from one strain of HCV, hereinafter referred to as CDC/HCV1, is sufficient to allow a viral taxonomist to identify other strains which fall within the species. As 25 described herein, we have discovered that HCV is a Flavivirus or Flavi-like virus. The morphology and composition of Flavivirus particles are known, and are discussed in Brinton (1986). Generally, with respect to morphology, Flaviviruses contain a central nucleocapsid 30 surrounded by a lipid bilayer. Virions are spherical and have a diameter of about 40-50 nm. Their cores are about 25-30 nm in diameter. Along the outer surface of the virion envelope are projections that are about 5-10 nm long with terminal knobs about 2 nm in diameter.

HCV encodes an epitope which is immunologically identifiable with an epitope in the HCV genome from which the cDNAs described herein are derived; preferably the epitope is encoded in a cDNA described herein. The 5 epitope is unique to HCV when compared to other known Flaviviruses. The uniqueness of the epitope may be determined by its immunological reactivity with HCV and lack of immunological reactivity with other Flavivirus species. Methods for determining immunological reactivity 10 are known in the art, for example, by radioimmunoassay, by Elisa assay, by hemagglutination, and several examples of suitable techniques for assays are provided herein.

In addition to the above, the following parameters are applicable, either alone or in combination, 15 in identifying a strain as HCV. Since HCV strains are evolutionarily related, it is expected that the overall homology of the genomes at the nucleotide level will be about 40% or greater, preferably about 60% or greater, and even more preferably about 80% or greater; and in addition 20 that there will be corresponding contiguous sequences of at least about 13 nucleotides. The correspondence between the putative HCV strain genomic sequence and the CDC/CH1 HCV cDNA sequence can be determined by techniques known in the art. For example, they can be determined by a direct 25 comparison of the sequence information of the polynucleotide from the putative HCV, and the HCV cDNA sequence(s) described herein. For example, also, they can be determined by hybridization of the polynucleotides under conditions which form stable duplexes between 30 homologous regions (for example, those which would be used prior to S<sub>1</sub> digestion), followed by digestion with single stranded specific nuclease(s), followed by size determination of the digested fragments.

Because of the evolutionary relationship of the 35 strains of HCV, putative HCV strains are identifiable by

their homology at the polypeptide level. Generally, HCV strains are more than about 40% homologous, preferably more than about 60% homologous, and even more preferably more than about 80% homologous at the polypeptide level.

- 5 The techniques for determining amino acid sequence homology are known in the art. For example, the amino acid sequence may be determined directly and compared to the sequences provided herein. For example also, the nucleotide sequence of the genomic material of the  
10 putative HCV may be determined (usually via a cDNA intermediate); the amino acid sequence encoded therein can be determined, and the corresponding regions compared.

As used herein, a polynucleotide "derived from" a designated sequence, for example, the HCV cDNA,  
15 particularly those exemplified in Figs. 1-32, or from an HCV genome, refers to a polynucleotide sequence which is comprised of a sequence of approximately at least about 6 nucleotides, is preferably at least about 8 nucleotides, is more preferably at least about 10-12 nucleotides, and  
20 even more preferably at least about 15-20 nucleotides corresponding, i.e., homologous to or complementary to, a region of the designated nucleotide sequence. Preferably, the sequence of the region from which the polynucleotide is derived is homologous to or complementary to a sequence  
25 which is unique to an HCV genome. Whether or not a sequence is unique to the HCV genome can be determined by techniques known to those of skill in the art. For example, the sequence can be compared to sequences in databanks, e.g., Genebank, to determine whether it is  
30 present in the uninfected host or other organisms. The sequence can also be compared to the known sequences of other viral agents, including those which are known to induce hepatitis, e.g., HAV, HBV, and HDV, and to other members of the Flaviviridae. The correspondence or non-  
35 correspondence of the derived sequence to other sequences

can also be determined by hybridization under the appropriate stringency conditions. Hybridization techniques for determining the complementarity of nucleic acid sequences are known in the art, and are discussed infra.

5 See also, for example, Maniatis et al. (1982). In addition, mismatches of duplex polynucleotides formed by hybridization can be determined by known techniques, including for example, digestion with a nuclease such as S1 that specifically digests single-stranded areas in 10 duplex polynucleotides. Regions from which typical DNA sequences may be "derived" include but are not limited to, for example, regions encoding specific epitopes, as well as non-transcribed and/or non-translated regions.

The derived polynucleotide is not necessarily 15 physically derived from the nucleotide sequence shown, but may be generated in any manner, including for example, chemical synthesis or DNA replication or reverse transcription or transcription, which are based on the information provided by the sequence of bases in the 20 region(s) from which the polynucleotide is derived. In addition, combinations of regions corresponding to that of the designated sequence may be modified in ways known in the art to be consistent with an intended use.

Similarly, a polypeptide or amino acid sequence 25 "derived from" a designated nucleic acid sequence, for example, the sequences in Figs. 1-32, or from an HCV genome, refers to a polypeptide having an amino acid sequence identical to that of a polypeptide encoded in the sequence, or a portion thereof wherein the portion 30 consists of at least 3-5 amino acids, and more preferably at least 8-10 amino acids, and even more preferably at least 11-15 amino acids, or which is immunologically identifiable with a polypeptide encoded in the sequence.

A recombinant or derived polypeptide is not 35 necessarily translated from a designated nucleic acid

sequence, for example, the sequences in Figs. 1-26, or from an HCV genome; it may be generated in any manner, including for example, chemical synthesis, or expression of a recombinant expression system, or isolation from 5 mutated HCV.

The term "recombinant polynucleotide" as used herein intends a polynucleotide of genomic, cDNA, semisynthetic, or synthetic origin which, by virtue of its origin or manipulation: (1) is not associated with all or 10 a portion of the polynucleotide with which it is associated in nature or in the form of a library; and/or (2) is linked to a polynucleotide other than that to which it is linked in nature.

The term "polynucleotide" as used herein refers 15 to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA, as well as double- and single stranded RNA. It also includes 20 modified, for example, by methylation and/or by capping, and unmodified forms of the polynucleotide.

As used herein, the term "HCV containing a sequence corresponding to a cDNA" means that the HCV contains a polynucleotide sequence which is homologous to 25 or complementary to a sequence in the designated DNA; the degree of homology or complementarity to the cDNA will be approximately 50% or greater, will preferably be at least about 70%, and even more preferably will be at least about 90%. The sequences which correspond will be at least 30 about 70 nucleotides, preferably at least about 80 nucleotides, and even more preferably at least about 90 nucleotides in length. The correspondence between the HCV sequence and the cDNA can be determined by techniques known in the art, including, for example, a direct 35 comparison of the sequenced material with the cDNAs

described, or hybridization and digestion with single strand nucleases, followed by size determination of the digested fragments.

The term "purified of viral polynucleotide" 5 refers to an HCV genome or fragment thereof which is essentially free, i.e., contains less than about 50%, preferably less than about 70%, and even more preferably less than about 90% of polypeptides with which the viral polynucleotide is naturally associated. Techniques for 10 purifying viral polynucleotides from viral particles are known in the art, and include for example, disruption of the particle with a chaotropic agent, and separation of the polynucleotide(s) and polypeptides by ion-exchange chromatography, affinity chromatography, and sedimentation 15 according to density.

The term "purified viral polypeptided" refers to an HCV polypeptide or fragment thereof which is essentially free, i.e., contains less than about 50%, preferably less than about 70%, and even more preferably 20 less than about 90%, of cellular components with which the viral polypeptide is naturally associated. Techniques for purifying viral polypeptides are known in the art, and examples of these techniques are discussed infra.

"Recombinant host cells", "host cells", "cells", 25 "cell lines", "cell cultures:", and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refer to cells which can be, or have been, used as recipients for recombinant vector or other transfer DNA, and include the progeny of 30 the original cell which has been transfected. It is understood that the progeny of a single parental cell may not necessarily be completely identical in morphology or in genomic or total DNA complement as the original parent, due to accidental or deliberate mutation. Progeny of the 35 parental cell which are sufficiently similar to the parent

to be characterized by the relevant property, such as the presence of a nucleotide sequence encoding a desired peptide, are included in the progeny intended by this definition, and are covered by the above terms.

5 A "replicon" is any genetic element, e.g., a plasmid, a chromosome, a virus, that behaves as an autonomous unit of polynucleotide replication within a cell; i.e., capable of replication under its own control.

10 A "vector" is a replicon in which another polynucleotide segment is attached, so as to bring about the replication and/or expression of the attached segment.

15 "Control sequence" refers to polynucleotide sequences which are necessary to effect the expression of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and terminators; in eukaryotes, generally, such control sequences include promoters, terminators and, in some instances, enhancers.

20 The term "control sequences" is intended to include, at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

25 "Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

30 An "open reading frame" (ORF) is a region of a polynucleotide sequence which encodes a polypeptide; this region may represent a portion of a coding sequence or a total coding sequence.

A "coding sequence" is a polynucleotide sequence which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include, but is not limited to mRNA, cDNA, and recombinant polynucleotide sequences.

"Immunologically identifiable with/as" refers to the presence of epitope(s) and polypeptides(s) which are also present in and are unique to the designated polypeptide(s), usually HCV proteins. Immunological identity may be determined by antibody binding and/or competition in binding; these techniques are known to those of average skill in the art, and are also illustrated infra. The uniqueness of an epitope can also be determined by computer searches of known data banks, e.g. Genebank, for the polynucleotide sequences which encode the epitope, and by amino acid sequence comparisons with other known proteins.

As used herein, "epitope" refers to an antigenic determinant of a polypeptide; an epitope could comprise 3 amino acids in a spatial conformation which is unique to the epitope, generally an epitope consists of at least 5 such amino acids, and more usually, consists of at least 8-10 such amino acids. Methods of determining the spatial conformation of amino acids are known in the art, and include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance.

A polypeptide is "immunologically reactive" with an antibody when it binds to an antibody due to antibody recognition of a specific epitope contained within the polypeptide. Immunological reactivity may be determined by antibody binding, more particularly by the kinetics of

antibody binding, and/or by competition in binding using as competitor(s) a known polypeptide(s) containing an epitope against which the antibody is directed. The techniques for determining whether a polypeptide is immunologically reactive with an antibody are known in the art.

As used herein, the term "immunogenic polypeptide containing an HCV epitope" includes naturally occurring HCV polypeptides or fragments thereof, as well 10 as polypeptides prepared by other means, for example, chemical synthesis, or the expression of the polypeptide in a recombinant organism.

The term "polypeptide" refers to a molecular chain of amino acids and does not refer to a specific 15 length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not refer to post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the 20 like.

"Transformation", as used herein, refers to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, direct uptake, transduction, or f-mating. The 25 exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host genome.

"Treatment" as used herein refers to prophylaxis and/or therapy.

An "individual", as used herein, refers to vertebrates, particularly members of the mammalian species, and includes but is not limited to domestic animals, sports animals, primates, and humans.

As used herein, the "plus strand" of a nucleic acid contains the sequence that encodes the polypeptide.

-26-

The "minus strand" contains a sequence which is complementary to that of the "plus strand".

As used herein, a "positive stranded genome" of a virus is one in which the genome, whether RNA or DNA, is 5 single-stranded and which encodes a viral polypeptide(s). Examples of positive stranded RNA viruses include Togaviridae, Coronaviridae, Retroviridae, Picornaviridae, and Caliciviridae. Included also, are the Flaviviridae, which were formerly classified as Togaviradae. See Fields 10 & Knipe (1986).

As used herein, "antibody containing body component" refers to a component of an individual's body which is a source of the antibodies of interest. Anti-body containing body components are known in the art, and 15 include but are not limited to, for example, plasma, serum, spinal fluid, lymph fluid, the external sections of the respiratory, intestinal, and genitourinary tracts, tears, saliva, milk, white blood cells, and myelomas.

As used herein, "purified HCV" refers to a 20 preparation of HCV which has been isolated from the cellular constituents with which the virus is normally associated, and from other types of viruses which may be present in the infected tissue. The techniques for isolating viruses are known to those of skill in the art, and 25 include, for example, centrifugation and affinity chromatography; a method of preparing purified HCV is discussed infra.

## II. Description of the Invention

30 The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Maniatis, Fitzsch & Sambrook,

-27-

MOLECULAR CLONING; A LABORATORY MANUAL (1982); DNA CLONING, VOLUMES I AND II (D.N. Glover ed. 1985); OLIGONUCLEOTIDE SYNTHESIS (M.J. Gait ed, 1984); NUCLEIC ACID HYBRIDIZATION (B.D. Hames & S.J. Higgins eds. 1984);  
5 TRANSCRIPTION AND TRANSLATION (B.D. Hames & S.J. Higgins eds. 1984); ANIMAL CELL CULTURE (R.I. Freshney ed. 1986); IMMobilized CELLS AND ENZYMES (IRL Press, 1986); B. Perbal, A PRACTICAL GUIDE TO MOLECULAR CLONING (1984);  
10 the series, METHODS IN ENZYMOLOGY (Academic Press, Inc.); GENE TRANSFER VECTORS FOR MAMMALIAN CELLS (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory), Methods in Enzymology Vol. 154 and Vol. 155 (Wu and Grossman, and Wu, eds., respectively), Mayer and Walker,  
15 eds. (1987), IMMUNOCHEMICAL METHODS IN CELL AND MOLECULAR BIOLOGY (Academic Press, London), Scopes, (1987), PROTEIN PURIFICATION: PRINCIPLES AND PRACTICE, Second Edition (Springer-Verlag, N.Y.), and HANDBOOK OF EXPERIMENTAL IMMUNOLOGY, VOLUMES I-IV (D.M. Weir and C. C. Blackwell eds  
20 1986).

20 All patents, patent applications, and publications mentioned herein, both supra and infra, are hereby incorporated herein by reference.

The useful materials and processes of the present invention are made possible by the provision of a family of closely homologous nucleotide sequences isolated from a cDNA library derived from nucleic acid sequences present in the plasma of an HCV infected chimpanzee. This family of nucleotide sequences is not of human or chimpanzee origin, since it hybridizes to neither human nor chimpanzee genomic DNA from uninfected individuals, since nucleotides of this family of sequences are present only in liver and plasma of chimpanzees with HCV infection, and since the sequence is not present in Genbank. In addition, the family of sequences shows no significant homology to sequences contained within the HBV genome.  
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30  
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-28-

The sequence of one member of the family, contained within clone 5-1-1, has one continuous open reading frame (ORF) which encodes a polypeptide of approximately 50 amino acids. Sera from HCV infected humans 5 contain antibodies which bind to this polypeptide, whereas sera from non-infected humans do not contain antibodies to this polypeptide. Finally, whereas the sera from uninfected chimpanzees do not contain antibodies to this polypeptide, the antibodies are induced in chimpanzees 10 following acute NANBH infection. Moreover, antibodies to this polypeptide are not detected in chimps and humans infected with HAV and HBV. By these criteria the sequence is a cDNA to a viral sequence, wherein the virus causes or is associated with NANBH; this cDNA sequence is shown in 15 Fig. 1. As discussed infra, the cDNA sequence in clone 5-1-1 differs from that of the other isolated cDNAs in that it contains 28 extra base pairs.

A composite of other identified members of the cDNA family, which were isolated using as a probe a 20 synthetic sequence equivalent to a fragment of the cDNA in clone 5-1-1, is shown in Fig. 3. A member of the cDNA family which was isolated using a synthetic sequence derived from the cDNA in clone 81 is shown in Fig. 5, and the composite of this sequence with that of clone 81 is 25 shown in Fig. 6. Other members of the cDNA family, including those present in clones 12f, 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, and 33g, 39c, 35f, 19g, 26g and 15e are described in 30 Section IV.A.. A composite of the cDNAs in these clones is described in Section IV.A.19, and shown in Fig. 32. The composite cDNA shows that it contains one continuous ORF, and thus encodes a polyprotein. This data is consistent with the suggestion, discussed infra., that HCV is a flavivirus or flavi-like virus.

-29-

The availability of this family of cDNAs shown in Figs. 1-32, inclusive, permits the construction of DNA probes and polypeptides useful in diagnosing NANBH due to HCV infection and in screening blood donors as well as 5 donated blood and blood products for infection. For example, from the sequences it is possible to synthesize DNA oligomers of about 8-10 nucleotides, or larger, which are useful as hybridization probes to detect the presence of the viral genome in, for example, sera of subjects 10 suspected of harboring the virus, or for screening donated blood for the presence of the virus. The family of cDNA sequences also allows the design and production of HCV specific polypeptides which are useful as diagnostic reagents for the presence of antibodies raised during NANBH. 15 Antibodies to purified polypeptides derived from the cDNAs may also be used to detect viral antigens in infected individuals and in blood.

Knowledge of these cDNA sequences also enable the design and production of polypeptides which may be 20 used as vaccines against HCV and also for the production of antibodies, which in turn may be used for protection against the disease, and/or for therapy of HCV infected individuals.

Moreover, the family of cDNA sequences enables 25 further characterization of the HCV genome.

Polynucleotide probes derived from these sequences may be used to screen cDNA libraries for additional overlapping cDNA sequences, which, in turn, may be used to obtain more overlapping sequences. Unless the genome is segmented and 30 the segments lack common sequences, this technique may be used to gain the sequence of the entire genome. However, if the genome is segmented, other segments of the genome can be obtained by repeating the lambda-gt11 serological screening procedure used to isolate the cDNA clones

-30-

described herein, or alternatively by isolating the genome from purified HCV particles.

The family of cDNA sequences and the polypeptides derived from these sequences, as well as antibodies directed against these polypeptides are also useful in the isolation and identification of the BB-NANBV agent(s). For example, antibodies directed against HCV epitopes contained in polypeptides derived from the cDNAs may be used in processes based upon affinity

chromatography to isolate the virus. Alternatively, the antibodies may be used to identify viral particles isolated by other techniques. The viral antigens and the genomic material within the isolated viral particles may then be further characterized.

The information obtained from further sequencing of the HCV genome(s), as well as from further characterization of the HCV antigens and characterization of the genome enables the design and synthesis of additional probes and polypeptides and antibodies which may be used for diagnosis, for prevention, and for therapy of HCV induced NANBH, and for screening for infected blood and blood-related products.

The availability of probes for HCV, including antigens and antibodies, and polynucleotides derived from the genome from which the family of cDNAs is derived also allows for the development of tissue culture systems which will be of major use in elucidating the biology of HCV. This in turn, may lead to the development of new treatment regimens based upon antiviral compounds which preferentially inhibit the replication of, or infection by HCV.

The method used to identify and isolate the etiologic agent for NANBH is novel, and it may be applicable to the identification and/or isolation of heretofore uncharacterized agents which contain a genome, and

which are associated with a variety of diseases, including those induced by viruses, viroids, bacteria, fungi and parasites. In this method, a cDNA library was created from the nucleic acids present in infected tissue from an 5 infected individual. The library was created in a vector which allowed the expression of polypeptides encoded in the cDNA. Clones of host cells containing the vector, which expressed an immunologically reactive fragment of a polypeptide of the etiologic agent, were selected by immunological screening of the expression products of the library with an antibody containing body component from another individual previously infected with the putative agent. The steps in the immunological screening technique included interacting the expression products of the cDNA 10 containing vectors with the antibody containing body component of a second infected individual, and detecting the formation of antibody-antigen complexes between the expression product(s) and antibodies of the second infected individual. The isolated clones are screened 15 further immunologically by interacting their expression products with the antibody containing body components of other individuals infected with the putative agent and with control individuals uninfected with the putative agent, and detecting the formation of antigen-antibody complexes with antibodies from the infected individuals; and the cDNA containing vectors which encode polypeptides 20 which react immunologically with antibodies from infected individuals and individuals suspected of being infected with the agent, but not with control individuals are isolated. The infected individuals used for the construction of the cDNA library, and for the immunological 25 screening need not be of the same species.

The cDNAs isolated as a result of this method, and their expression products, and antibodies directed 30 against the expression products, are useful in character- 35

izing and/or capturing the etiologic agent. As described in more detail infra, this method has been used successfully to isolate a family of cDNAs derived from the HCV genome.

5

### II.A. Preparation of the cDNA Sequence

Pooled serum from a chimpanzee with chronic HCV infection and containing a high titer of the virus, i.e., at least  $10^6$  chimp infectious doses/ml (CID/ml) was used 10 to isolate viral particles; nucleic acids isolated from these particles was used as the template in the construction of a cDNA library to the viral genome. The procedures for isolation of putative HCV particles and for constructing the cDNA library in lambda-gt11 is discussed 15 in Section IV.A.1. Lambda-gt11 is a vector that has been developed specifically to express inserted cDNAs as fusion polypeptides with beta-galactosidase and to screen large numbers of recombinant phage with specific antisera raised against a defined antigen. The lambda-gt11 cDNA library 20 generated from a cDNA pool containing cDNA of approximate mean size of 200 base pairs was screened for encoded epitopes that could bind specifically with sera derived from patients who had previously experienced NANB hepatitis. Huynh, T.V. et al. (1985). Approximately  $10^6$  25 phages were screened, and five positive phages were identified, purified, and then tested for specificity of binding to sera from different humans and chimpanzees previously infected with the HCV agent. One of the phages, 5-1-1, bound 5 of the 8 human sera tested. This 30 binding appeared selective for sera derived from patients with prior NANB hepatitis infections since 7 normal blood donor sera did not exhibit such binding.

The sequence of the cDNA in recombinant phage 5-1-1 was determined, and is shown in Fig. 1. The 35 polypeptide encoded by this cloned cDNA, which is in the

same translational frame as the N-terminal beta-Galactosidase moiety of the fusion polypeptide is shown above the nucleotide sequence. This translational ORF, therefore, encodes an epitope(s) specifically recognized  
5 by sera from patients with NANB hepatitis infections.

The availability of the cDNA in recombinant phage 5-1-1 has allowed for the isolation of other clones containing additional segments and/or alternative segments of cDNA to the viral genome. The lambda-gt11 cDNA library  
10 described supra, was screened using a synthetic polynucleotide derived from the sequence of the cloned 5-1-1 cDNA. This screening yielded three other clones, which were identified as 81, 1-2 and 91; the cDNAs contained within these clones were sequenced. See Sections  
15 IV.A.3. and IV.A.4. The homologies between the four independent clones are shown in Fig. 2, where the homologies are indicated by the vertical lines. Sequences of nucleotides present uniquely in clones 5-1-1, 81, and 91 are indicated by small letters.  
20

The cloned cDNAs present in recombinant phages in clones 5-1-1, 81, 1-2, and 91 are highly homologous, and differ in only two regions. First, nucleotide number 67 in clone 1-2 is a thymidine, whereas the other three clones contain a cytidine residue in this position. This  
25 substitution, however, does not alter the nature of the encoded amino acid.

The second difference between the clones is that clone 5-1-1 contains 28 base pairs at its 5'-terminus which are not present in the other clones. The extra  
30 sequence may be a 5'-terminal cloning artifact; 5'-terminal cloning artifacts are commonly observed in the products of cDNA methods.

Synthetic sequences derived from the 5'-region and the 3'-region of the HCV cDNA in clone 81 were used to  
35 screen and isolate cDNAs from the lambda-gt11 NANBV cDNA

-34-

library, which overlapped clone 81 cDNA (Section IV.A.5.). The sequences of the resulting cDNAs, which are in clone 36 and clone 32, respectively, are shown in Fig. 5 and Fig. 7.

5           Similarly, a synthetic polynucleotide based on the 5'-region of clone 36 was used to screen and isolate cDNAs from the lambda gt-11 NANBV cDNA library which overlapped clone 36 cDNA (Section IV.A.8.). A purified clone of recombinant phage-containing cDNA which hybridized to the synthetic polynucleotide probe was named clone 10 35 and the NANBV cDNA sequence contained within this clone is shown in Fig. 8.

15          By utilizing the technique of isolating overlapping cDNA sequences, clones containing additional upstream and downstream HCV cDNA sequences have been obtained. The isolation of these clones, is described infra in Section IV.A.

20          Analysis of the nucleotide sequences of the HCV cDNAs encoded within the isolated clones show that the composite cDNA contains one long continuous ORF. Fig. 26 shows the sequence of the composite cDNA from these clones, along with the putative HCV polypeptide encoded therein.

25          The description of the method to retrieve the cDNA sequences is mostly of historical interest. The resultant sequences (and their complements) are provided herein, and the sequences, or any portion thereof, could be prepared using synthetic methods, or by a combination of synthetic methods with retrieval of partial sequences 30 using methods similar to those described herein.

             Lambda-gt11 strains replicated from the HCV cDNA library and from clones 5-1-1, 81, 1-2 and 91 have been deposited under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), 12301 Parklawn

-35-

Dr., Rockville, Maryland 20852, and have been assigned the following Accession Numbers.

	<u>lambda-gt11</u>	<u>ATCC No.</u>	<u>Deposit Date</u>
5	HCV cDNA library	40394	1 Dec. 1987
	clone 81	40388	17 Nov. 1987
	clone 91	40389	17 Nov. 1987
	clone 1-2	40390	17 Nov. 1987
	clone 5-1-1	40391	18 Nov. 1987

10

Upon allowance and issuance of this application as a United States Patent, all restriction on availability of these deposits will be irrevocably removed; and access to the designated deposits will be available during pendency 15 of the above-named application to one determined by the Commissioner to be entitled thereto under 37 CFR 1.14 and 35 USC 1.22. Moreover, the designated deposits will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request 20 for the deposit; or for the enforceable life of the U.S. patent, whichever is longer. These deposits and other deposited materials mentioned herein are intended for convenience only, and are not required to practice the present invention in view of the description here. The 25 HCV cDNA sequences in all of the deposited materials are incorporated herein by reference.

The description above, of "walking" the genome by isolating overlapping cDNA sequences from the HCV lambda gt-11 library provides one method by which cDNAs 30 corresponding to the entire HCV genome may be isolated. However, given the information provided herein, other methods for isolating these cDNAs are obvious to one of skill in the art. Some of these methods are described in Section IV.A., infra.

### II.B. Preparation of Viral Polypeptides and Fragments

The availability of cDNA sequences, either those isolated by utilizing the cDNA sequences in Figs. 1-32, as discussed infra, as well as the cDNA sequences in these figures, permits the construction of expression vectors encoding antigenically active regions of the polypeptide encoded in either strand. These antigenically active regions may be derived from coat or envelope antigens or from core antigens, including, for example, polynucleotide binding proteins, polynucleotide polymerase(s), and other viral proteins required for the replication and/or assembly of the virus particle. Fragments encoding the desired polypeptides are derived from the cDNA clones using conventional restriction digestion or by synthetic methods, and are ligated into vectors which may, for example, contain portions of fusion sequences such as beta-Galactosidase or superoxide dismutase (SOD), preferably SOD. Methods and vectors which are useful for the production of polypeptides which contain fusion sequences of SOD are described in European Patent Office Publication number 0196056, published October 1, 1986. Vectors encoding fusion polypeptides of SOD and HCV polypeptides, i.e., NANB<sub>5-1-1</sub>, NANB<sub>81</sub>, and C100-3, which is encoded in a composite of HCV cDNAs, are described in Sections IV.B.1, IV.B.2, and IV.B.4, respectively. Any desired portion of the HCV cDNA containing an open reading frame, in either sense strand, can be obtained as a recombinant polypeptide; such as a mature or fusion protein; alternatively, a polypeptide encoded in the cDNA can be provided by chemical synthesis.

The DNA encoding the desired polypeptide, whether in fused or mature form, and whether or not containing a signal sequence to permit secretion, may be ligated into expression vectors suitable for any convenient host. Both eukaryotic and prokaryotic host

systems are presently used in forming recombinant polypeptides, and a summary of some of the more common control systems and host cell lines is given in Section III.A., infra. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification may be by techniques known in the art, for example, salt fractionation, chromatography on ion exchange resins, affinity chromatography, centrifugation, and the like. See, for example, Methods in Enzymology for a variety of methods for purifying proteins. Such polypeptides can be used as diagnostics, or those which give rise to neutralizing antibodies may be formulated into vaccines. Antibodies raised against these polypeptides can also be used as diagnostics, or for passive immunotherapy. In addition, as discussed in Section II.J. herein below, antibodies to these polypeptides are useful for isolating and identifying HCV particles.

The HCV antigens may also be isolated from HCV virions. The virions may be grown in HCV infected cells in tissue culture, or in an infected host.

#### II.C. Preparation of Antigenic Polypeptides and Conjugation with Carrier

An antigenic region of a polypeptide is generally relatively small--typically 8 to 10 amino acids or less in length. Fragments of as few as 5 amino acids may characterize an antigenic region. These segments may correspond to regions of HCV antigen. Accordingly, using the cDNAs of HCV as a basis, DNAs encoding short segments of HCV polypeptides can be expressed recombinantly either as fusion proteins, or as isolated polypeptides. In addition, short amino acid sequences can be conveniently obtained by chemical synthesis. In instances wherein the synthesized polypeptide is correctly configured so as to

provide the correct epitope, but is too small to be immunogenic, the polypeptide may be linked to a suitable carrier.

A number of techniques for obtaining such linkage are known in the art, including the formation of disulfide linkages using N-succinimidyl-3-(2-pyridyl-thio)propionate (SPDP) and succinimidyl 4-(N-maleimido-methyl)cyclohexane-1-carboxylate (SMCC) obtained from Pierce Company, Rockford, Illinois, (if the peptide lacks a sulfhydryl group, this can be provided by addition of a cysteine residue.) These reagents create a disulfide linkage between themselves and peptide cysteine residues on one protein and an amide linkage through the epsilon-amino on a lysine, or other free amino group in the other. A variety of such disulfide/amide-forming agents are known. See, for example, Immun. Rev. (1982) 62:185. Other bifunctional coupling agents form a thioether rather than a disulfide linkage. Many of these thio-ether-forming agents are commercially available and include reactive esters of 6-maleimidocaproic acid, 2-bromoacetic acid, 2-iodoacetic acid, 4-(N-maleimido-methyl)cyclohexane-1-carboxylic acid, and the like. The carboxyl groups can be activated by combining them with succinimide or 1-hydroxyl-2-nitro-4-sulfonic acid, sodium salt. The foregoing list is not meant to be exhaustive, and modifications of the named compounds can clearly be used.

Any carrier may be used which does not itself induce the production of antibodies harmful to the host. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins; polysaccharides, such as latex functionalized sepharose, agarose, cellulose, cellulose beads and the like; polymeric amino acids, such as polyglutamic acid, polylysine, and the like; amino acid copolymers; and inactive virus particles, see, for

example, section II.D. Especially useful protein substrates are serum albumins, keyhole limpet hemocyanin, immunoglobulin molecules, thyroglobulin, ovalbumin, tetanus toxoid, and other proteins well known to those skilled in the art.

II.D. Preparation of Hybrid Particle Immunogens Containing HCV Epitopes

The immunogenicity of the epitopes of HCV may also be enhanced by preparing them in mammalian or yeast systems fused with or assembled with particle-forming proteins such as, for example, that associated with hepatitis B surface antigen. Constructs wherein the NANBV epitope is linked directly to the particle-forming protein coding sequences produce hybrids which are immunogenic with respect to the HCV epitope. In addition, all of the vectors prepared include epitopes specific to HBV, having various degrees of immunogenicity, such as, for example, the pre-S peptide. Thus, particles constructed from particle forming protein which include HCV sequences are immunogenic with respect to HCV and HBV.

Hepatitis surface antigen (HBSAg) has been shown to be formed and assembled into particles in S. cerevisiae (Valenzuela et al. (1982)), as well as in, for example, mammalian cells (Valenzuela, P., et al. (1984)). The formation of such particles has been shown to enhance the immunogenicity of the monomer subunit. The constructs may also include the immunodominant epitope of HBSAg, comprising the 55 amino acids of the presurface (pre-S) region. Neurath et al. (1984). Constructs of the pre-S-HBSAg particle expressible in yeast are disclosed in EPO 174,444, published March 19, 1986; hybrids including heterologous viral sequences for yeast expression are disclosed in EPO 175,261, published March 26, 1986. Both applications are assigned to the herein assignee, and are

-40-

incorporated herein by reference. These constructs may also be expressed in mammalian cells such as Chinese hamster ovary (CHO) cells using an SV40-dihydrofolate reductase vector (Michelle et al. (1984)).

5 In addition, portions of the particle-forming protein coding sequence may be replaced with codons encoding an HCV epitope. In this replacement, regions which are not required to mediate the aggregation of the units to form immunogenic particles in yeast or mammals can be deleted, thus eliminating additional HBV antigenic sites from competition with the HCV epitope.

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#### II.E. Preparation of Vaccines

Vaccines may be prepared from one or more immunogenic polypeptides derived from HCV cDNA as well as from the cDNA sequences in the Figs. 1-32, or from the HCV genome to which they correspond. The observed homology between HCV and Flaviviruses provides information concerning the polypeptides which are likely to be most effective as vaccines, as well as the regions of the genome in which they are encoded. The general structure of the Flavivirus genome is discussed in Rice et al (1986). The flavivirus genomic RNA is believed to be the only virus-specific mRNA species, and it is translated into the three viral structural proteins, i.e., C, M, and E, as well as two large nonstructural proteins, NV4 and NV5, and a complex set of smaller nonstructural proteins. It is known that major neutralizing epitopes for Flaviviruses reside in the E (envelope) protein (Roehrig (1986)). The corresponding HCV E gene and polypeptide encoding region can be predicted, based upon the homology to Flaviviruses. Thus, vaccines may be comprised of recombinant polypeptides containing epitopes of HCV E. These polypeptides may be expressed in bacteria, yeast, or mammalian cells, or alternatively may be isolated from

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-41-

viral preparations. It is also anticipated that the other structural proteins may also contain epitopes which give rise to protective anti-HCV antibodies. Thus, polypeptides containing the epitopes of E, C, and M may 5 also be used, whether singly or in combination, in HCV vaccines.

In addition to the above, it has been shown that immunization with NS1 (nonstructural protein 1), results in protection against yellow fever (Schlesinger et al 10 (1986)). This is true even though the immunization does not give rise to neutralizing antibodies. Thus, particularly since this protein appears to be highly conserved among Flaviviruses, it is likely that HCV NS1 will also be protective against HCV infection. Moreover, 15 it also shows that nonstructural proteins may provide protection against viral pathogenicity, even if they do not cause the production of neutralizing antibodies.

In view of the above, multivalent vaccines against HCV may be comprised of one or more structural 20 proteins, and/or one or more nonstructural proteins. These vaccines may be comprised of, for example, recombinant HCV polypeptides and/or polypeptides isolated from the virions. In addition, it may be possible to use inactivated HCV in vaccines; inactivation may be by the 25 preparation of viral lysates, or by other means known in the art to cause inactivation of Flaviviruses, for example, treatment with organic solvents or detergents, or treatment with formalin. Moreover, vaccines may also be prepared from attenuated HCV strains. The preparation of 30 attenuated HCV strains is described infra.

It is known that some of the proteins in Flaviviruses contain highly conserved regions, thus, some immunological cross-reactivity is expected between HCV and other Flaviviruses. It is possible that shared epitopes 35 between the Flaviviruses and HCV will give rise to

protective antibodies against one or more of the disorders caused by these pathogenic agents. Thus, it may be possible to design multipurpose vaccines based upon this knowledge.

5       The preparation of vaccines which contain an immunogenic polypeptide(s) as active ingredients, is known to one skilled in the art. Typically, such vaccines are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or  
10      suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified, or the protein encapsulated in liposomes. The active immunogenic ingredients are often mixed with excipients which are pharmaceutically acceptable and compatible with the active  
15      ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering  
20      agents, and/or adjuvants which enhance the effectiveness of the vaccine. Examples of adjuvants which may be effective include but are not limited to: aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine  
25      (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid  
30      A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion. The effectiveness of an adjuvant may be determined by measuring the amount of antibodies directed against an immunogenic polypeptide containing an HCV antigenic sequence resulting from administration of this polypeptide  
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in vaccines which are also comprised of the various adjuvants.

The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

The proteins may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

#### II.F. Dosage and Administration of Vaccines

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount

as will be prophylactically and/or therapeutically effective. The quantity to be administered, which is generally in the range of 5 micrograms to 250 micrograms of antigen per dose, depends on the subject to be treated, capacity 5 of the subject's immune system to synthesize antibodies, and the degree of protection desired. Precise amounts of active ingredient required to be administered may depend on the judgment of the practitioner and may be peculiar to each subject.

10 The vaccine may be given in a single dose schedule, or preferably in a multiple dose schedule. A multiple dose schedule is one in which a primary course of vaccination may be with 1-10 separate doses, followed by other doses given at subsequent time intervals required to 15 maintain and or reenforce the immune response, for example, at 1-4 months for a second dose, and if needed, a subsequent dose(s) after several months. The dosage regimen will also, at least in part, be determined by the need of the individual and be dependent upon the judgment 20 of the practitioner.

In addition, the vaccine containing the immunogenic HCV antigen(s) may be administered in conjunction with other immunoregulatory agents, for example, immune globulins.

25 **II.G. Preparation of Antibodies Against HCV Epitopes**  
The immunogenic polypeptides prepared as described above are used to produce antibodies, both polyclonal and monoclonal. If polyclonal antibodies are 30 desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunized with an immunogenic polypeptide bearing an HCV epitope(s). Serum from the immunized animal is collected and treated according to known procedures. If serum containing polyclonal antibodies to 35 an HCV epitope contains antibodies to other antigens, the

-45-

polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art, see for example, Mayer and Walker (1987).

5        Alternatively, polyclonal antibodies may be isolated from a mammal which has been previously infected with HCV. An example of a method for purifying antibodies to HCV epitopes from serum from an infected individual, based upon affinity chromatography and utilizing a fusion 10 polypeptide of SOD and a polypeptide encoded within cDNA clone 5-1-1, is presented in Section V.E.

Monoclonal antibodies directed against HCV epitopes can also be readily produced by one skilled in the art. The general methodology for making monoclonal 15 antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., M. 20 Schreier et al. (1980); Hammerling et al. (1981); Kennett et al. (1980); see also, U.S. Patent Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,466,917; 4,472,500; 4,491,632; and 4,493,890. Panels of monoclonal antibodies produced against HCV epitopes can be screened for various 25 properties; i.e., for isotype, epitope affinity, etc.

Antibodies, both monoclonal and polyclonal, which are directed against HCV epitopes are particularly useful in diagnosis, and those which are neutralizing are useful in passive immunotherapy. Monoclonal antibodies, 30 in particular, may be used to raise anti-idiotype antibodies.

Anti-idiotype antibodies are immunoglobulins which carry an "internal image" of the antigen of the infectious agent against which protection is desired.

See, for example, Nisonoff, A., et al. (1981) and Dreesman et al. (1985).

Techniques for raising anti-idiotype antibodies are known in the art. See, for example, Grzych (1985), MacNamara et al. (1984), and Uytdehaag et al. (1985). These anti-idiotype antibodies may also be useful for treatment of NANBH, as well as for an elucidation of the immunogenic regions of HCV antigens.

10 II.H. Diagnostic Oligonucleotide Probes and Kits

Using the disclosed portions of the isolated HCV cDNAs as a basis, including those in Figs. 1-32, oligomers of approximately 8 nucleotides or more can be prepared, either by excision or synthetically, which hybridize with the HCV genome and are useful in identification of the viral agent(s), further characterization of the viral genome(s), as well as in detection of the virus(es) in diseased individuals. The probes for HCV polynucleotides (natural or derived) are a length which allows the detection of unique viral sequences by hybridization. While 6-8 nucleotides may be a workable length, sequences of 10-12 nucleotides are preferred, and about 20 nucleotides appears optimal. Preferably, these sequences will derive from regions which lack heterogeneity. These probes can be prepared using routine methods, including automated oligonucleotide synthetic methods. Among useful probes, for example, are the clone 5-1-1 and the additional clones disclosed herein, as well as the various oligomers useful in probing cDNA libraries, set forth below. A complement to any unique portion of the HCV genome will be satisfactory. For use as probes, complete complementarity is desirable, though it may be unnecessary as the length of the fragment is increased.

For use of such probes as diagnostics, the biological sample to be analyzed, such as blood or serum, is

treated, if desired, to extract the nucleic acids contained therein. The resulting nucleic acid from the sample may be subjected to gel electrophoresis or other size separation techniques; alternatively, the nucleic acid sample may be dot blotted without size separation. 5 The probes are then labeled. Suitable labels, and methods for labeling probes are known in the art, and include, for example, radioactive labels incorporated by nick translation or kinasing, biotin, fluorescent probes, and chemiluminescent probes. The nucleic acids extracted from 10 the sample are then treated with the labeled probe under hybridization conditions of suitable stringencies.

The probes can be made completely complementary to the HCV genome. Therefore, usually high stringency 15 conditions are desirable in order to prevent false positives. However, conditions of high stringency should only be used if the probes are complementary to regions of the viral genome which lack heterogeneity. The stringency of hybridization is determined by a number of factors during 20 hybridization and during the washing procedure, including temperature, ionic strength, length of time, and concentration of formamide. These factors are outlined in, for example, Maniatis, T. (1982).

Generally, it is expected that the HCV genome 25 sequences will be present in serum of infected individuals at relatively low levels, i.e., at approximately  $10^2$ - $10^3$  sequences per ml. This level may require that amplification techniques be used in hybridization assays. Such 30 techniques are known in the art. For example, the Enzo Biochemical Corporation "Bio-Bridge" system uses terminal deoxynucleotide transferase to add unmodified 3'-poly-dT-tails to a DNA probe. The poly dT-tailed probe is hybridized to the target nucleotide sequence, and then to a 35 biotin-modified poly-A. PCT application 84/03520 and EPA124221 describe a DNA hybridization assay in which: (1)

analyte is annealed to a single-stranded DNA probe that is complementary to an enzyme-labeled oligonucleotide; and (2) the resulting tailed duplex is hybridized to an enzyme-labeled oligonucleotide. EPA 204510 describes a 5 DNA hybridization assay in which analyte DNA is contacted with a probe that has a tail, such as a poly-dT tail, an amplifier strand that has a sequence that hybridizes to the tail of the probe, such as a poly-A sequence, and which is capable of binding a plurality of labeled strands. A particularly desirable technique may first 10 involve amplification of the target HCV sequences in sera approximately 10,000 fold, i.e., to approximately  $10^6$  sequences/ml. This may be accomplished, for example, by the technique of Saiki et al. (1986). The amplified 15 sequence(s) may then be detected using a hybridization assay which is described in co-pending U.S. Application, Attorney Docket No. 2300-0171, which was filed 15 October 1987, is assigned to the herein assignee, and is hereby incorporated herein by reference. This hybridization assay, 20 which should detect sequences at the level of  $10^6$ /ml utilizes nucleic acid multimers which bind to single-stranded analyte nucleic acid, and which also bind to a multiplicity of single-stranded labeled oligonucleotides. A suitable solution phase sandwich assay which may be used 25 with labeled polynucleotide probes, and the methods for the preparation of probes is described in EPO 225,807, published June 16, 1987, which is assigned to the herein assignee, and which is hereby incorporated herein by reference.

30 The probes can be packaged into diagnostic kits. Diagnostic kits include the probe DNA, which may be labeled; alternatively, the probe DNA may be unlabeled and the ingredients for labeling may be included in the kit. The kit may also contain other suitably packaged reagents 35 and materials needed for the particular hybridization

protocol, for example, standards, as well as instructions for conducting the test.

### II.I. Immunoassay and Diagnostic Kits

Both the polypeptides which react immuno logically with serum containing HCV antibodies, for example, those derived from or encoded within the clones described in Section IV.A., and composites thereof, (see section IV.A.) and the antibodies raised against the HCV specific epitopes in these polypeptides, see for example Section IV.E, are useful in immunoassays to detect presence of HCV antibodies, or the presence of the virus and/or viral antigens, in biological samples, including for example, blood or serum samples. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. For example, the immunoassay may utilize one viral antigen, for example, a polypeptide derived from any of the clones containing HCV cDNA described in Section IV.A., or from the composite cDNAs derived from the cDNAs in these clones, or from the HCV genome from which the cDNA in these clones is derived; alternatively, the immunoassay may use a combination of viral antigens derived from these sources. It may use, for example, a monoclonal antibody directed towards a viral epitope(s), a combination of monoclonal antibodies directed towards one viral antigen, monoclonal antibodies directed towards different viral antigens, polyclonal antibodies directed towards the same viral antigen, or polyclonal antibodies directed towards different viral antigens. Protocols may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive,

-50-

or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

5       The Flavivirus model for HCV allows predictions regarding the likely location of diagnostic epitopes for the virion structural proteins. The C, pre-M, M, and E domains are all likely to contain epitopes of significant potential for detecting viral antigens, and particularly 10 for diagnosis. Similarly, domains of the nonstructural proteins are expected to contain important diagnostic epitopes (e.g., NS5 encoding a putative polymerase; and NS1 encoding a putative complement-binding antigen). Recombinant polypeptides, or viral polypeptides, which 15 include epitopes from these specific domains may be useful for the detection of viral antibodies in infectious blood donors and infected patients.

In addition, antibodies directed against the E and/or M proteins can be used in immunoassays for the 20 detection of viral antigens in patients with HCV caused NANBH, and in infectious blood donors. Moreover, these antibodies will be extremely useful in detecting acute-phase donors and patients.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by 25 packaging the appropriate materials, including the polypeptides of the invention containing HCV epitopes or antibodies directed against HCV epitopes in suitable containers, along with the remaining reagents and material- 30 als required for the conduct of the assay, as well as a suitable set of assay instructions.

II.J. Further Characterization of the HCV Genome, Virions, and Viral Antigens Using Probes Derived From cDNA to the Viral Genome

The HCV cDNA sequence information in the clones described in Section IV.A., as shown in Figs. 1-32, inclusive, may be used to gain further information on the sequence of the HCV genome, and for identification and isolation of the HCV agent, and thus will aid in its characterization including the nature of the genome, the structure of the viral particle, and the nature of the antigens of which it is composed. This information, in turn, can lead to additional polynucleotide probes, polypeptides derived from the HCV genome, and antibodies directed against HCV epitopes which would be useful for the diagnosis and/or treatment of HCV caused NANBH.

The cDNA sequence information in the above-mentioned clones is useful for the design of probes for the isolation of additional cDNA sequences which are derived from as yet undefined regions of the HCV genome(s) from which the cDNAs in clones described in Section IV.A. are derived. For example, labeled probes containing a sequence of approximately 8 or more nucleotides, and preferably 20 or more nucleotides, which are derived from regions close to the 5'-termini or 3'-termini of the family of HCV cDNA sequences shown in Figs. 1, 3, 6, 9, 14 and 32 may be used to isolate overlapping cDNA sequences from HCV cDNA libraries. These sequences which overlap the cDNAs in the above-mentioned clones, but which also contain sequences derived from regions of the genome from which the cDNA in the above mentioned clones are not derived, may then be used to synthesize probes for identification of other overlapping fragments which do not necessarily overlap the cDNAs in the clones described in Section IV.A. Unless the HCV genome is segmented and the segments lack common sequences, it is possible to sequence

the entire viral genome(s) utilizing the technique of isolation of overlapping cDNAs derived from the viral genome(s). Although it is unlikely, if the genome is a segmented genome which lacks common sequences, the 5 sequence of the genome can be determined by serologically screening lambda-gt11 HCV cDNA libraries, as used to isolate clone 5-1-1, sequencing cDNA isolates, and using the isolated cDNAs to isolate overlapping fragments, using the technique described for the isolation and sequencing 10 of the clones described in Section IV.A. Alternatively, characterization of the genomic segments could be from the viral genome(s) isolated from purified HCV particles. Methods for purifying HCV particles and for detecting them during the purification procedure are described herein, 15 infra. Procedures for isolating polynucleotide genomes from viral particles are known in the art, and one procedure which may be used is shown in Example IV.A.1. The isolated genomic segments could then be cloned and sequenced. Thus, with the information provided herein, it 20 is possible to clone and sequence the HCV genome(s) irrespective of their nature.

Methods for constructing cDNA libraries are known in the art, and are discussed supra and infra; a method for the construction of HCV cDNA libraries in 25 lambda-gt11 is discussed infra in Section IV.A. However, cDNA libraries which are useful for screening with nucleic acid probes may also be constructed in other vectors known in the art, for example, lambda-gt10 (Huynh et al. (1985)). The HCV derived cDNA detected by the probes 30 derived from the cDNAs in Figs. 1-32, and from the probes synthesized from polynucleotides derived from these cDNAs, may be isolated from the clone by digestion of the isolated polynucleotide with the appropriate restriction enzyme(s), and sequenced. See, for example, Section 35 IV.A.3. and IV.A.4. for the techniques used for the

isolation and sequencing of HCV cDNA which overlaps HCV cDNA in clone 5-1-1, Sections IV.A.5-IV.A.7 for the isolation and sequencing of HCV cDNA which overlaps that in clone 81, and Section IV.A.8 and IV.A.9 for the 5 isolation and sequencing of a clone which overlaps another clone (clone 36), which overlaps clone 81.

The sequence information derived from these overlapping HCV cDNAs is useful for determining areas of homology and heterogeneity within the viral genome(s), 10 which could indicate the presence of different strains of the genome, and/or of populations of defective particles. It is also useful for the design of hybridization probes to detect HCV or HCV antigens or HCV nucleic acids in biological samples, and during the isolation of HCV 15 (discussed infra), utilizing the techniques described in Section II.G. Moreover, the overlapping cDNAs may be used to create expression vectors for polypeptides derived from the HCV genome(s) which also encode the polypeptides encoded in clones 5-1-1, 36, 81, 91, and 1-2, and in the 20 other clones described in Section IV.A. The techniques for the creation of these polypeptides containing HCV epitopes, and for antibodies directed against HCV epitopes contained within them, as well as their uses, are analogous to those described for polypeptides derived from 25 NANBV cDNA sequences contained within clones 5-1-1, 32, 35, 36, 1-2, 81, and 91, discussed supra and infra.

Encoded within the family of cDNA sequences contained within clones 5-1-1, 32, 35, 36, 81, 91, 1-2, and the other clones described in Section IV.A. are 30 antigen(s) containing epitopes which appear to be unique to HCV; i.e., antibodies directed against these antigens are absent from individuals infected with HAV or HBV, and from individuals not infected with HCV (see the serological data presented in Section IV.B.). Moreover, a 35 comparison of the sequence information of these cDNAs with

the sequences of HAV, HBV, HDV, and with the genomic sequences in Genebank indicates that minimal homology exists between these cDNAs and the polynucleotide sequences of those sources. Thus, antibodies directed against the 5 antigens encoded within the cDNAs of these clones may be used to identify BB-NANBV particles isolated from infected individuals. In addition, they are also useful for the isolation of NANBH agent(s).

HCV particles may be isolated from the sera from 10 BB-NANBV infected individuals or from cell cultures by any of the methods known in the art, including for example, techniques based on size discrimination such as sedimentation or exclusion methods, or techniques based on density such as ultracentrifugation in density gradients, or 15 precipitation with agents such as polyethylene glycol, or chromatography on a variety of materials such as anionic or cationic exchange materials, and materials which bind due to hydrophobicity, as well as affinity columns. During the isolation procedure the presence of HCV may be 20 detected by hybridization analysis of the extracted genome, using probes derived from the HCV cDNAs described supra, or by immunoassay (see Section II.I.) utilizing as probes antibodies directed against HCV antigens encoded within the family of cDNA sequences shown in Figs. 1-32, 25 and also directed against HCV antigens encoded within the overlapping HCV cDNA sequences discussed supra. The antibodies may be monoclonal, or polyclonal, and it may be desirable to purify the antibodies before their use in the immunoassay. A purification procedure for polyclonal 30 antibodies directed against antigen(s) encoded within clone 5-1-1 is described in Section IV.E; analogous purification procedures may be utilized for antibodies directed against other HCV antigens.

Antibodies directed against HCV antigens encoded 35 within the family of cDNAs shown in Figs. 1-32, as well as

those encoded within overlapping HCV cDNAs, which are affixed to solid supports are useful for the isolation of HCV by immunoaffinity chromatography. Techniques for immunoaffinity chromatography are known in the art, 5 including techniques for affixing antibodies to solid supports so that they retain their immunoselective activity; the techniques may be those in which the antibodies are adsorbed to the support (see, for example, Kurstak in ENZYME IMMUNODIAGNOSIS, page 31-37), as well as those in 10 which the antibodies are covalently linked to the support. Generally, the techniques are similar to those used for covalent linking of antigens to a solid support, which are generally described in Section II.C.; however, spacer groups may be included in the bifunctional coupling agents 15 so that the antigen binding site of the antibody remains accessible.

During the purification procedure the presence of HCV may be detected and/or verified by nucleic acid hybridization, utilizing as probes polynucleotides derived 20 from the family of HCV cDNA sequences shown in Figs. 1-32, as well as from overlapping HCV cDNA sequences, described supra. In this case, the fractions are treated under conditions which would cause the disruption of viral particles, for example, with detergents in the presence of 25 chelating agents, and the presence of viral nucleic acid determined by hybridization techniques described in Section II.H. Further confirmation that the isolated particles are the agents which induce HCV may be obtained by infecting chimpanzees with the isolated virus 30 particles, followed by a determination of whether the symptoms of NANBH result from the infection.

Viral particles from the purified preparations may then be further characterized. The genomic nucleic acid has been purified. Based upon its sensitivity to 35 RNase, and not DNase I, it appears that the virus is

composed of an RNA genome. See Example IV.C.2., *infra*. The strandedness and circularity or non-circularity can be determined by techniques known in the art, including, for example, its visualization by electron microscopy, its migration in density gradients, and its sedimentation characteristics. Based upon the hybridization of the captured HCV genome to the negative strands of HCV cDNAs, it appears that HCV may be comprised of a positive stranded RNA genome (see Section IV.H.1). Techniques such as these are described in, for example, *METHODS IN ENZYMOLOGY*. In addition, the purified nucleic acid can be cloned and sequenced by known techniques, including reverse transcription since the genomic material is RNA. See, for example, Maniatis (1982), and Glover (1985).

Utilizing the nucleic acid derived from the viral particles, it is possible to sequence the entire genome, whether or not it is segmented.

Examination of the homology of the polypeptide encoded within the continuous ORF of combined clones 14i through 39c (see Fig. 26), shows that the HCV polypeptide contains regions of homology with the corresponding proteins in conserved regions of flaviviruses. An example of this is described in Section IV.H.3. This finding has many important ramifications. First, this evidence, in conjunction with the results which show that HCV contains a positive-stranded genome, the size of which is approximately 10,000 nucleotides, is consistent with the suggestion that HCV is a flavivirus, or flavi-like virus. Generally, flavivirus virions and their genomes have a relatively consistent structure and organization, which are known. See Rice et al. (1986), and Brinton, M.A. (1988). Thus, the structural genes encoding the polypeptides C, pre-M/M, and E may be located in the 5'-terminus of the genome upstream of clone 14i. Moreover, using the comparison with other flaviviruses, predictions

as to the precise location of the sequences encoding these proteins can be made.

Isolation of the sequences upstream of those in clone 14i may be accomplished in a number of ways which, given the information herein, would be obvious to one of skill in the art. For example, the genome "walking" technique, may be used to isolate other sequences which are 5' to those in clone 14i, but which overlap that clone; this in turn leads to the isolation of additional sequences. This technique has been amply demonstrated infra, in Section IV.A.. For example, also, it is known that the flaviviruses have conserved epitopes and regions of conserved nucleic acid sequences. Polynucleotides containing the conserved sequences may be used as probes which bind the HCV genome, thus allowing its isolation. In addition, these conserved sequences, in conjunction with those derived from the HCV cDNAs shown in Fig. 22, may be used to design primers for use in systems which amplify the genome sequences upstream of those in clone 14i, using polymerase chain reaction technology. An example of this is described infra.

The structure of the HCV may also be determined and its components isolated. The morphology and size may be determined by, for example, electron microscopy. The identification and localization of specific viral polypeptide antigens such as coat or envelope antigens, or internal antigens, such as nucleic acid binding proteins, core antigens, and polynucleotide polymerase(s) may also be determined by, for example, determining whether the antigens are present as major or minor viral components, as well as by utilizing antibodies directed against the specific antigens encoded within isolated cDNAs as probes. This information is useful in the design of vaccines; for example, it may be preferable to include an exterior antigen in a vaccine preparation. Multivalent vaccines

may be comprised of, for example, a polypeptide derived from the genome encoding a structural protein, for example, E, as well as a polypeptide from another portion of the genome, for example, a nonstructural or structural 5 polypeptide.

#### II.K. Cell Culture Systems and Animal Model Systems for HCV Replication

The suggestion that HCV is a flavivirus or flavi-like virus also provides information on methods for growing HCV. The term "flavi-like" means that the virus shows a significant amount of homology to the known conserved regions of flaviviruses and that the majority of the genome is a single ORF. Methods for culturing 10 flaviviruses are known to those of skill in the art (See, for example, the reviews by Brinton (1986) and Stollar, V. (1980)). Generally, suitable cells or cell lines for culturing HCV may include those known to support 15 Flavivirus replication, for example, the following: monkey kidney cell lines (e.g. MK<sub>2</sub>, VERO); porcine kidney cell lines (e.g. PS); baby hamster kidney cell lines (e.g. BHK); murine macrophage cell lines (e.g., P388D1, MK1, Mm1); human macrophage cell lines (e.g., U-937); human peripheral blood leukocytes; human adherent monocytes; 20 hepatocytes or hepatocyte cell lines (e.g., HUH7, HEPG2); embryos or embryonic cells (e.g., chick embryo fibroblasts); or cell lines derived from invertebrates, preferably from insects (e.g. drosophila cell lines), or more preferably from arthropods, for example, mosquito 25 cell lines (e.g., A. Albopictus, Aedes aegypti, Cutex tritaeniorhynchus) or tick cell lines (e.g. RML-14 Dermacentor parumapertus).

It is possible that primary hepatocytes can be cultured, and then infected with HCV; or alternatively, 30 the hepatocyte cultures could be derived from the livers

of infected individuals (e.g., humans or chimpanzees). The latter case is an example of a cell which is infected in vivo being passaged in vitro. In addition, various immortalization methods can be used to obtain cell-lines 5 derived from hepatocyte cultures. For example, primary liver cultures (before and after enrichment of the hepatocyte population) may be fused to a variety of cells to maintain stability. For example, also, cultures may be infected with transforming viruses, or transfected with 10 transforming genes in order to create permanent or semipermanent cell lines. In addition, for example, cells in liver cultures may be fused to established cell lines (e.g., HepG2 ). Methods for cell fusion are known in the art, and include, for example, the use of fusion agents 15 such as polyethylene glycol, Sendai Virus, and Epstein-Barr virus.

As discussed above, HCV is a Flavivirus or Flavi-like virus. Therefore, it is probable that HCV infection of cell lines may be accomplished by techniques 20 known in the art for infecting cells with Flaviviruses. These include, for example, incubating the cells with viral preparations under conditions which allow viral entry into the cell. In addition, it may be possible to obtain viral production by transfecting the cells with 25 isolated viral polynucleotides. It is known that Togavirus and Flavivirus RNAs are infectious in a variety of vertebrate cell lines (Pfefferkorn and Shapiro (1974)), and in a mosquito cell line (Peleg (1969)). Methods for transfecting tissue culture cells with RNA 30 duplexes, positive stranded RNAs, and DNAs (including cDNAs) are known in the art, and include, for example, techniques which use electroporation, and precipitation with DEAE-Dextran or calcium phosphate. An abundant source of HCV RNA can be obtained by performing in vitro 35 transcription of an HCV cDNA corresponding to the complete

-60-

genome. Transfection with this material, or with cloned HCV cDNA should result in viral replication and the in vitro propagation of the virus.

In addition to cultured cells, animal model  
5 systems may be used for viral replication; animal systems in which flaviviruses are known to those of skill in the art (See, for example, the review by Monath (1986)). Thus, HCV replication may occur not only in chimpanzees, but also in, for example, marmosets and suckling mice.

10

### II.L. Screening for Anti-Viral Agents for HCV

The availability of cell culture and animal model systems for HCV also makes possible screening for anti-viral agents which inhibit HCV replication, and  
15 particularly for those agents which preferentially allow cell growth and multiplication while inhibiting viral replication. These screening methods are known by those of skill in the art. Generally, the anti-viral agents are tested at a variety of concentrations, for their effect on  
20 preventing viral replication in cell culture systems which support viral replication, and then for an inhibition of infectivity or of viral pathogenicity (and a low level of toxicity) in an animal model system.

The methods and compositions provided herein for  
25 detecting HCV antigens and HCV polynucleotides are useful for screening of anti-viral agents in that they provide an alternative, and perhaps more sensitive means, for detecting the agent's effect on viral replication than the cell plaque assay or ID<sub>50</sub> assay. For example, the HCV-  
30 polynucleotide probes described herein may be used to quantitate the amount of viral nucleic acid produced in a cell culture. This could be accomplished, for example, by hybridization or competition hybridization of the infected cell nucleic acids with a labeled HCV-polynucleotide probe. For example, also, anti-HCV antibodies may be used  
35

to identify and quantitate HCV antigen(s) in the cell culture utilizing the immunoassays described herein. In addition, since it may be desirable to quantitate HCV antigens in the infected cell culture by a competition assay, the polypeptides encoded within the HCV cDNAs described herein are useful in these competition assays. Generally, a recombinant HCV polypeptide derived from the HCV cDNA would be labeled, and the inhibition of binding of this labeled polypeptide to an HCV polypeptide due to the antigen produced in the cell culture system would be monitored. Moreover, these techniques are particularly useful in cases where the HCV may be able to replicate in a cell line without causing cell death.

15 II.M. Preparation of Attenuated Strains of HCV

In addition to the above, utilizing the tissue culture systems and/or animal model systems, it may be possible to isolate attenuated strains of HCV. These strains would be suitable for vaccines, or for the isolation of viral antigens. Attenuated strains are isolatable after multiple passages in cell culture and/or an animal model. Detection of an attenuated strain in an infected cell or individual is achievable by techniques known in the art, and could include, for example, the use of antibodies to one or more epitopes encoded in HCV as a probe or the use of a polynucleotide containing an HCV sequence of at least about 8 nucleotides as a probe. Alternatively, or in addition, an attenuated strain may be constructed utilizing the genomic information of HCV provided herein, and utilizing recombinant techniques. Generally, one would attempt to delete a region of the genome encoding, for example, a polypeptide related to pathogenicity, but which allows viral replication. In addition, the genome construction would allow the expression of an epitope which gives rise to neutralizing

antibodies for HCV. The altered genome could then be utilized to transform cells which allow HCV replication, and the cells grown under conditions to allow viral replication. Attenuated HCV strains are useful not only for vaccine purposes, but also as sources for the commercial production of viral antigens, since the processing of these viruses would require less stringent protection measures for the employees involved in viral production and/or the production of viral products.

10

### III. General Methods

The general techniques used in extracting the genome from a virus, preparing and probing a cDNA library, sequencing clones, constructing expression vectors, transforming cells, performing immunological assays such as radioimmunoassays and ELISA assays, for growing cells in culture, and the like are known in the art and laboratory manuals are available describing these techniques. However, as a general guide, the following sets forth some sources currently available for such procedures, and for materials useful in carrying them out.

#### III.A. Hosts and Expression Control Sequences

Both prokaryotic and eukaryotic host cells may be used for expression of desired coding sequences when appropriate control sequences which are compatible with the designated host are used. Among prokaryotic hosts, E. coli is most frequently used. Expression control sequences for prokaryotes include promoters, optionally containing operator portions, and ribosome binding sites. Transfer vectors compatible with prokaryotic hosts are commonly derived from, for example, pBR322, a plasmid containing operons conferring ampicillin and tetracycline resistance, and the various pUC vectors, which also contain sequences conferring antibiotic resistance mark-

ers. These markers may be used to obtain successful transformants by selection. Commonly used prokaryotic control sequences include the Beta-lactamase (penicillinase) and lactose promoter systems (Chang et al. 5 (1977)), the tryptophan (trp) promoter system (Goeddel et al. (1980)) and the lambda-derived P<sub>L</sub> promoter and N gene ribosome binding site (Shimatake et al. (1981)) and the hybrid tac promoter (De Boer et al. (1983)) derived from sequences of the trp and lac UV5 promoters. The foregoing 10 systems are particularly compatible with E. coli; if desired, other prokaryotic hosts such as strains of Bacillus or Pseudomonas may be used, with corresponding control sequences.

Eukaryotic hosts include yeast and mammalian 15 cells in culture systems. Saccharomyces cerevisiae and Saccharomyces carlsbergensis are the most commonly used yeast hosts, and are convenient fungal hosts. Yeast compatible vectors carry markers which permit selection of successful transformants by conferring prototrophy to 20 auxotrophic mutants or resistance to heavy metals on wild-type strains. Yeast compatible vectors may employ the 2 micron origin of replication (Broach et al. (1983)), the combination of CEN3 and ARS1 or other means for assuring replication, such as sequences which will result in incorporation of an appropriate fragment into the host cell 25 genome. Control sequences for yeast vectors are known in the art and include promoters for the synthesis of glycolytic enzymes (Hess et al. (1968); Holland et al. (1978)), including the promoter for 3 phosphoglycerate kinase (Hitzeman (1980)). Terminators may also be included, such as those derived from the enolase gene 30 (Holland (1981)). Particularly useful control systems are those which comprise the glyceraldehyde-3 phosphate dehydrogenase (GAPDH) promoter or alcohol dehydrogenase 35 (ADH) regulatable promoter, terminators also derived from

-64-

GAPDH, and if secretion is desired, leader sequence from yeast alpha factor. In addition, the transcriptional regulatory region and the transcriptional initiation region which are operably linked may be such that they are 5 not naturally associated in the wild-type organism. These systems are described in detail in EPO 120,551, published October 3, 1984; EPO 116,201, published August 22, 1984; and EPO 164,556, published December 18, 1985, all of which are assigned to the herein assignee, and are hereby 10 incorporated herein by reference.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including HeLa cells, Chinese hamster 15 ovary (CHO) cells, baby hamster kidney (BHK) cells, and a number of other cell lines. Suitable promoters for mammalian cells are also known in the art and include viral promoters such as that from Simian Virus 40 (SV40) (Fiers (1978)), Rous sarcoma virus (RSV), adenovirus (ADV), and 20 bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences and poly A addition sequences; enhancer sequences which increase expression may also be included, and sequences which cause amplification of the gene may also be desirable. These sequences 25 are known in the art. Vectors suitable for replication in mammalian cells may include viral replicons, or sequences which insure integration of the appropriate sequences encoding NANBV epitopes into the host genome.

30 III.B. Transformations

Transformation may be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus and transducing a host cell with the virus, and by direct 35 uptake of the polynucleotide. The transformation

procedure used depends upon the host to be transformed. For example, transformation of the *E. coli* host cells with lambda-gt11 containing BB-NANBV sequences is discussed in the Example section, infra. Bacterial transformation by direct uptake generally employs treatment with calcium or rubidium chloride (Cohen (1972); Maniatis (1982)). Yeast transformation by direct uptake may be carried out using the method of Hinnen et al. (1978). Mammalian transformations by direct uptake may be conducted using the calcium phosphate precipitation method of Graham and Van der Eb (1978), or the various known modifications thereof.

### III.C. Vector Construction

Vector construction employs techniques which are known in the art. Site-specific DNA cleavage is performed by treating with suitable restriction enzymes under conditions which generally are specified by the manufacturer of these commercially available enzymes. In general, about 1 microgram of plasmid or DNA sequence is cleaved by 1 unit of enzyme in about 20 microliters buffer solution by incubation of 1-2 hr at 37° C. After incubation with the restriction enzyme, protein is removed by phenol/chloroform extraction and the DNA recovered by precipitation with ethanol. The cleaved fragments may be separated using polyacrylamide or agarose gel electrophoresis techniques, according to the general procedures found in Methods in Enzymology (1980) 65:499-560.

Sticky ended cleavage fragments may be blunt ended using *E. coli* DNA polymerase I (Klenow) in the presence of the appropriate deoxynucleotide triphosphates (dNTPs) present in the mixture. Treatment with S1 nuclease may also be used, resulting in the hydrolysis of any single stranded DNA portions.

Ligations are carried out using standard buffer and temperature conditions using T4 DNA ligase and ATP;

sticky end ligations require less ATP and less ligase than blunt end ligations. When vector fragments are used as part of a ligation mixture, the vector fragment is often treated with bacterial alkaline phosphatase (BAP) or calf 5 intestinal alkaline phosphatase to remove the 5'-phosphate and thus prevent religation of the vector; alternatively, restriction enzyme digestion of unwanted fragments can be used to prevent ligation.

10 Ligation mixtures are transformed into suitable cloning hosts, such as E. coli, and successful transformants selected by, for example, antibiotic resistance, and screened for the correct construction.

#### III.D. Construction of Desired DNA Sequences

15 Synthetic oligonucleotides may be prepared using an automated oligonucleotide synthesizer as described by Warner (1984). If desired the synthetic strands may be labeled with <sup>32</sup>P by treatment with polynucleotide kinase in the presence of <sup>32</sup>P-ATP, using standard conditions for 20 the reaction.

DNA sequences, including those isolated from cDNA libraries, may be modified by known techniques, including, for example site directed mutagenesis, as described by Zoller (1982). Briefly, the DNA to be 25 modified is packaged into phage as a single stranded sequence, and converted to a double stranded DNA with DNA polymerase using, as a primer, a synthetic oligonucleotide complementary to the portion of the DNA to be modified, and having the desired modification included in its own 30 sequence. The resulting double stranded DNA is transformed into a phage supporting host bacterium. Cultures of the transformed bacteria, which contain 35 replications of each strand of the phage, are plated in agar to obtain plaques. Theoretically, 50% of the new plaques contain phage having the mutated sequence, and the

-67-

remaining 50% have the original sequence. Replicates of the plaques are hybridized to labeled synthetic probe at temperatures and conditions which permit hybridization with the correct strand, but not with the unmodified 5 sequence. The sequences which have been identified by hybridization are recovered and cloned.

### III.E. Hybridization with Probe

DNA libraries may be probed using the procedure 10 of Grunstein and Hogness (1975). Briefly, in this procedure, the DNA to be probed is immobilized on nitro-cellulose filters, denatured, and prehybridized with a buffer containing 0-50% formamide, 0.75 M NaCl, 75 mM Na citrate, 0.02% (wt/v) each of bovine serum albumin, poly-15 vinyl pyrrolidone, and Ficoll, 50 mM Na Phosphate (pH 6.5), 0.1% SDS, and 100 micrograms/ml carrier denatured DNA. The percentage of formamide in the buffer, as well as the time and temperature conditions of the prehybridization and subsequent hybridization steps 20 depends on the stringency required. Oligomeric probes which require lower stringency conditions are generally used with low percentages of formamide, lower temperatures, and longer hybridization times. Probes containing more than 30 or 40 nucleotides such as those 25 derived from cDNA or genomic sequences generally employ higher temperatures, e.g., about 40-42°C, and a high percentage, e.g., 50%, formamide. Following prehybridization, 5'-<sup>32</sup>P-labeled oligonucleotide probe is added to the buffer, and the filters are incubated in this 30 mixture under hybridization conditions. After washing, the treated filters are subjected to autoradiography to show the location of the hybridized probe; DNA in corresponding locations on the original agar plates is used as the source of the desired DNA.

-68-

### III.F. Verification of Construction and Sequencing

For routine vector constructions, ligation mixtures are transformed into E. coli strain HB101 or other suitable host, and successful transformants selected  
5 by antibiotic resistance or other markers. Plasmids from the transformants are then prepared according to the method of Clewell et al. (1969), usually following chloramphenicol amplification (Clewell (1972)). The DNA is isolated and analyzed, usually by restriction enzyme  
10 analysis and/or sequencing. Sequencing may be by the dideoxy method of Sanger et al. (1977) as further described by Messing et al. (1981), or by the method of Maxam et al. (1980). Problems with band compression, which are sometimes observed in GC rich regions, were  
15 overcome by use of T-deazoguanosine according to Barr et al. (1986).

### III.G. Enzyme Linked Immunosorbent Assay

The enzyme-linked immunosorbent assay (ELISA)  
20 can be used to measure either antigen or antibody concentrations. This method depends upon conjugation of an enzyme to either an antigen or an antibody, and uses the bound enzyme activity as a quantitative label. To measure antibody, the known antigen is fixed to a solid  
25 phase (e.g., a microplate or plastic cup), incubated with test serum dilutions, washed, incubated with anti-immunoglobulin labeled with an enzyme, and washed again. Enzymes suitable for labeling are known in the art, and include, for example, horseradish peroxidase. Enzyme  
30 activity bound to the solid phase is measured by adding the specific substrate, and determining product formation or substrate utilization colorimetrically. The enzyme activity bound is a direct function of the amount of antibody bound.

To measure antigen, a known specific antibody is fixed to the solid phase, the test material containing antigen is added, after an incubation the solid phase is washed, and a second enzyme-labeled antibody is added.

- 5 After washing, substrate is added, and enzyme activity is estimated colorimetrically, and related to antigen concentration.

#### IV. Examples

10 Described below are examples of the present invention which are provided only for illustrative purposes, and not to limit the scope of the present invention. In light of the present disclosure, numerous embodiments within the scope of the claims will be apparent to those of ordinary skill in the art. The procedures set forth, for example, in Sections IV.A. may, if desired, be repeated but need not be, as techniques are available for construction of the desired nucleotide sequences based on the information provided by the invention. Expression 15 is exemplified in E. coli; however, other systems are available as set forth more fully in Section III.A. Additional epitopes derived from the genomic structure may also be produced, and used to generate antibodies as set forth below.

25

##### IV.A. Preparation, Isolation and Sequencing of HCV cDNA

###### IV.A.1. Preparation of HCV cDNA

The source of NANB agent was a plasma pool 30 derived from a chimpanzee with chronic NANBH. The chimpanzee had been experimentally infected with blood from another chimpanzee with chronic NANBH resulting from infection with HCV in a contaminated batch of factor 8 concentrate derived from pooled human sera. The 35 chimpanzee plasma pool was made by combining many

-70-

individual plasma samples containing high levels of alanine aminotransferase activity; this activity results from hepatic injury due to the HCV infection. Since 1 ml of a  $10^{-6}$  dilution of this pooled serum given i.v. caused 5 NANBH in another chimpanzee, its CID was at least  $10^6$ /ml, i.e., it had a high infectious virus titer.

A cDNA library from the high titer plasma pool was generated as follows. First, viral particles were isolated from the plasma; a 90 ml aliquot was diluted with 10 310 ml of a solution containing 50 mM Tris-HCl, pH 8.0, 1mM EDTA, 100 mM NaCl. Debris was removed by centrifugation for 20 min at 15,000 x g at  $20^{\circ}\text{C}$ . Viral particles in the resulting supernatant were then pelleted by 15 centrifugation in a Beckman SW28 rotor at 28,000 rpm for 5 hours at  $20^{\circ}\text{C}$ . To release the viral genome, the particles were disrupted by suspending the pellets in 15 ml solution containing 1% sodium dodecyl sulfate (SDS), 10 mM EDTA, 10 mM Tris-HCl, pH 7.5, also containing 2 mg/ml proteinase k, followed by incubation at  $45^{\circ}\text{C}$  for 90 min. Nucleic acids 20 were isolated by adding 0.8 micrograms MS2 bacteriophage RNA as carrier, and extracting the mixture four times with a 1:1 mixture of phenol:chloroform (phenol saturated with 0.5M Tris-HCl, pH 7.5, 0.1% (v/v) beta-mercaptoethanol, 0.1% (w/v) hydroxyquinolone, followed by extraction two 25 times with chloroform. The aqueous phase was concentrated with 1-butanol prior to precipitation with 2.5 volumes absolute ethanol overnight at  $-20^{\circ}\text{C}$ . Nucleic acid was recovered by centrifugation in a Beckman SW41 rotor at 40,000 rpm for 90 min at  $4^{\circ}\text{C}$ , and dissolved in water that 30 had been treated with 0.05% (v/v) diethylpyrocarbonate and autoclaved.

Nucleic acid obtained by the above procedure (<2 micrograms) was denatured with 17.5 mM  $\text{CH}_3\text{HgOH}$ ; cDNA was synthesized using this denatured nucleic acid as template, 35 and was cloned into the EcoRI site of phage lambda-gt11

using methods described by Huynh (1985), except that random primers replaced oligo(dT) 12-18 during the synthesis of the first cDNA strand by reverse transcriptase (Taylor et al. (1976)). The resulting 5 double stranded cDNAs were fractionated according to size on a Sepharose CL-4B column; eluted material of approximate mean size 400, 300, 200, and 100 base-pairs were pooled into cDNA pools 1, 2, 3, and 4, respectively. The lambda-gt11 cDNA library was generated from the cDNA 10 in pool 3.

The lambda-gt11 cDNA library generated from pool 3 was screened for epitopes that could bind specifically with serum derived from a patient who had previously experienced NANBH. About  $10^6$  phage were screened with 15 patient sera using the methods of Huynh et al. (1985), except that bound human antibody was detected with sheep anti-human Ig antisera that had been radio-labeled with  $^{125}\text{I}$ . Five positive phages were identified and purified. The five positive phages were then tested for specificity 20 of binding to sera from 8 different humans previously infected with the NANBH agent, using the same method. Four of the phage encoded a polypeptide that reacted immunologically with only one human serum, i.e., the one 25 that was used for primary screening of the phage library. The fifth phage (5-1-1) encoded a polypeptide that reacted immunologically with 5 of 8 of the sera tested. Moreover, this polypeptide did not react immunologically with sera from 7 normal blood donors. Therefore, it appears that 30 clone 5-1-1 encodes a polypeptide which is specifically recognized immunologically by sera from NANB patients.

IV.A.2. Sequences of the HCV cDNA in Recombinant Phage 5-1-1, and of the Polypeptide Encoded Within the Sequence.

The cDNA in recombinant phage 5-1-1 was 35 sequenced by the method of Sanger et al. (1977). Es-

-72-

sentially, the cDNA was excised with EcoRI, isolated by size fractionation using gel electrophoresis. The EcoRI restriction fragments were subcloned into the M13 vectors, mp18 and mp19 (Messing (1983)) and sequenced using the 5 dideoxychain termination method of Sanger et al. (1977). The sequence obtained is shown in Fig. 1.

The polypeptide encoded in Fig. 1 that is encoded in the HCV cDNA is in the same translational frame as the N-terminal beta-galactosidase moiety to which it is fused. As shown in Section IV.A., the translational open 10 reading frame (ORF) of 5-1-1 encodes epitope(s) specifically recognized by sera from patients and chimpanzees with NANBH infections.

15 IV.A.3. Isolation of Overlapping HCV cDNA to cDNA in Clone 5-1-1.

Overlapping HCV cDNA to the cDNA in clone 5-1-1 was obtained by screening the same lambda-gt11 library, created as described in Section IV.A.1., with a synthetic 20 polynucleotide derived from the sequence of the HCV cDNA in clones 5-1-1, as shown in Fig. 1. The sequence of the polynucleotide used for screening was:

5'-TCC CTT GCT CGA TGT ACG GTA AGT GCT GAG AGC  
25 ACT CTT CCA TCT CAT CGA ACT CTC GGT AGA GGA CTT CCC TGT  
CAG GT-3'.

The lambda-gt11 library was screened with this probe, using the method described in Huynh (1985). Approximately 30 1 in 50,000 clones hybridized with the probe. Three clones which contained cDNAs which hybridized with the synthetic probe have been numbered 81, 1-2, and 91.

IV.A.4. Nucleotide Sequences of Overlapping HCV cDNAs to cDNA in Clone 5-1-1.

The nucleotide sequences of the three cDNAs in clones 81, 1-2, and 91 were determined essentially as in 5 Section IV.A.2. The sequences of these clones relative to the HCV cDNA sequence in phage 5-1-1 is shown in Fig. 2, which shows the strand encoding the detected HCV epitope, and where the homologies in the nucleotide sequences are indicated by vertical lines between the sequences.

10 The sequences of the cloned HCV cDNAs are highly homologous in the overlapping regions (see Fig. 2). However, there are differences in two regions. Nucleotide 67 in clone 1-2 is a thymidine, whereas the other three clones contain a cytidine residue in this position. It 15 should be noted, however, that the same amino acid is encoded when either C or T occupies this position.

The second difference is that clone 5-1-1 contains 28 base pairs which are not present in the other three clones. These base pairs occur at the start of the 20 cDNA sequence in 5-1-1, and are indicated by small letters. Based on radioimmunoassay data, which is discussed infra in Section IV.D., it is possible that an HCV epitope may be encoded in this 28 bp region.

The absence of the 28 base pairs of 5-1-1 from 25 clones 81, 1-2, and 91 may mean that the cDNA in these clones were derived from defective HCV genomes; alternatively, the 28 bp region could be a terminal artifact in clone 5-1-1.

The sequences of small letters in the nucleotide 30 sequence of clones 81 and 91 simply indicate that these sequences have not been found in other cDNAs because cDNAs overlapping these regions were not yet isolated.

A composite HCV cDNA sequence derived from overlapping cDNAs in clones 5-1-1, 81, 1-2 and 91 is shown in 35 Fig. 3. However, in this figure the unique 28 base pairs

-74-

of clone 5-1-1 are omitted. The figure also shows the sequence of the polypeptide encoded within the ORF of the composite HCV cDNA.

5 IV.A.5. Isolation of Overlapping HCV cDNAs to cDNA in Clone 81.

The isolation of HCV cDNA sequences upstream of, and which overlap those in clone 81 cDNA was accomplished as follows. The lambda-gt11 cDNA library prepared as 10 described in Section IV.A.1. was screened by hybridization with a synthetic polynucleotide probe which was homologous to a 5' terminal sequence of clone 81. The sequence of clone 81 is presented in Fig. 4. The sequence of the synthetic polynucleotide used for screening was:

15  
5' CTG TCA GGT ATG ATT GCC GGC TTC CCG GAC 3'.

The methods were essentially as described in Huynh (1985), except that the library filters were given two washes 20 under stringent conditions, i.e., the washes were in 5 x SSC, 0.1% SDS at 55°C for 30 minutes each. Approximately 1 in 50,000 clones hybridized with the probe. A positive recombinant phage which contained cDNA which hybridized with the sequence was isolated and purified. This phage 25 has been numbered clone 36.

Downstream cDNA sequences, which overlaps the carboxyl-end sequences in clone 81 cDNA were isolated using a procedure similar to that for the isolation of upstream cDNA sequences, except that a synthetic 30 oligonucleotide probe was prepared which is homologous to a 3' terminal sequence of clone 81. The sequence of the synthetic polynucleotide used for screening was:

5' TTT GGC TAG TGG TTA GTG GGC TGG TGA CAG 3'

A positive recombinant phage, which contained cDNA which hybridized with this latter sequence was isolated and purified, and has been numbered clone 32.

5 IV.A.6. Nucleotide Sequence of HCV cDNA in Clone 36.

The nucleotide sequence of the cDNA in clone 36 was determined essentially as described in Section IV.A.2. The double-stranded sequence of this cDNA, its region of overlap with the HCV cDNA in clone 81, and the polypeptide encoded by the ORF are shown in Fig. 5.

The ORF in clone 36 is in the same translational frame as the HCV antigen encoded in clone 81. Thus, in combination, the ORFs in clones 36 and 81 encode a polypeptide that represents part of a large HCV antigen.

15 The sequence of this putative HCV polypeptide and the double stranded DNA sequence encoding it, which is derived from the combined ORFs of the HCV cDNAs of clones 36 and 81, is shown in Fig. 6.

20 IV.A.7 Nucleotide Sequences of HCV cDNA in Clone 32

The nucleotide sequence of the cDNA in clone 32 was determined essentially as was that described in Section IV.A.2 for the sequence of clone 5-1-1. The sequence data indicated that the cDNA in clone 32 recombinant phage 25 was derived from two different sources. One fragment of the cDNA was comprised of 418 nucleotides derived from the HCV genome; the other fragment was comprised of 172 nucleotides derived from the bacteriophage MS2 genome, which had been used as a carrier during the preparation of 30 the lambda gt11 plasma cDNA library.

The sequence of the cDNA in clone 32 corresponding to that of the HCV genome is shown in Fig. 7. The region of the sequences that overlaps that of clone 81, and the polypeptide encoded by the ORF are also indicated 35 in the figure. This sequence contains one continuous ORF

-76-

that is in the same translational frame as the HCV antigen encoded by clone 81.

IV.A.8 Isolation of Overlapping HCV cDNA to cDNA in Clone

5 36

The isolation of HCV cDNA sequences upstream of, and which overlap those in clone 36 cDNA was accomplished as described in Section IV.A.5, for those which overlap clone 81 cDNA, except that the synthetic polynucleotide 10 was based on the 5'-region of clone 36. The sequence of the synthetic polynucleotide used for screening was:

5' AAG CCA CCG TGT GCG CTA GGG CTC AAG CCC 3'

15 Approximately 1 in 50,000 clones hybridized with the probe. The isolated, purified clone of recombinant phage which contained cDNA which hybridized to this sequence was named clone 35.

20 IV.A.9 Nucleotide Sequence of HCV cDNA in Clone 35

The nucleotide sequence of the cDNA in clone 35 was determined essentially as described in Section IV.A.2. The sequence, its region of overlap with that of the cDNA in clone 36, and the putative polypeptide encoded therein, 25 are shown in Fig. 8.

Clone 35 apparently contains a single, continuous ORF that encodes a polypeptide in the same translational frame as that encoded by clone 36, clone 81, and clone 32. Fig. 9 shows the sequence of the long 30 continuous ORF that extends through clones 35, 36, 81, and 32, along with the putative HCV polypeptide encoded therein. This combined sequence has been confirmed using other independent cDNA clones derived from the same lambda gt11 cDNA library.

IV.A.10. Isolation of Overlapping HCV cDNA to cDNA in Clone 35

The isolation of HCV cDNA sequences upstream of, and which overlap those in clone 35 cDNA was accomplished 5 as described in Section IV.A.8, for those which overlap clone 36 cDNA, except that the synthetic polynucleotide was based on the 5'-region of clone 35. The sequence of the synthetic polynucleotide used for screening was:

10            5' CAG GAT GCT GTC TCC CGC ACT CAA CGT 3'

Approximately 1 in 50,000 clones hybridized with the probe. The isolated, purified clone of recombinant phage 15 which contained cDNA which hybridized to this sequence was named clone 37b.

IV.A.11. Nucleotide Sequence of HCV in Clone 37b

The nucleotide sequence of the cDNA in clone 37b was determined essentially as described in Section IV.A.2. 20 The sequence, its region of overlap with that of the cDNA in clone 35, and the putative polypeptide encoded therein, are shown in Fig. 10.

The 5'-terminal nucleotide of clone 35 is a T, whereas the corresponding nucleotide in clone 37b is an A. 25 The cDNAs from three other independent clones which were isolated during the procedure in which clone 37b was isolated, described in Section IV.A.10, have also been sequenced. The cDNAs from these clones also contain an A in this position. Thus, the 5'-terminal T in clone 35 may 30 be an artefact of the cloning procedure. It is known that artefacts often arise at the 5'-termini of cDNA molecules.

Clone 37b apparently contains one continuous ORF which encodes a polypeptide which is a continuation of the polypeptide encoded in the ORF which extends through the 35 overlapping clones 35, 36, 81 and 32.

-78-

IV.A.12 Isolation of Overlapping HCV cDNA to cDNA in Clone 32

The isolation of HCV cDNA sequences downstream of clone 32 was accomplished as follows. First, clone cla 5 was isolated utilizing a synthetic hybridization probe which was based on the nucleotide sequence of the HCV cDNA sequence in clone 32. The method was essentially that described in Section IV.A.5, except that the sequence of the synthetic probe was:

10

5' AGT GCA GTG GAT GAA CCG GCT GAT AGC CTT 3'.

Utilizing the nucleotide sequence from clone cla, another 15 synthetic nucleotide was synthesized which had the sequence:

5' TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT 3'.

Screening of the lambda gt11 library using the clone cla 20 derived sequence as probe yielded approximately 1 in 50,000 positive colonies. An isolated, purified clone which hybridized with this probe was named clone 33b.

IV.A.13 Nucleotide Sequence of HCV cDNA in Clone 33b

25 The nucleotide sequence of the cDNA in clone 33b was determined essentially as described in Section IV.A.2. The sequence, its region of overlap with that of the cDNA in clone 32, and the putative polypeptide encoded therein, are shown in Fig. 11.

30 Clone 33b apparently contains one continuous ORF which is an extension of the ORFs in overlapping clones 37b, 35, 36, 81 and 32. The polypeptide encoded in clone 33b is in the same translational frame as that encoded in the extended ORF of these overlapping clones.

35

-79-

IV.A.14 Isolation of Overlapping HCV cDNAs to cDNA Clone 37b and to cDNA in Clone 33b

In order to isolate HCV cDNAs which overlap the cDNAs in clone 37b and in clone 33b, the following 5 synthetic oligonucleotide probes, which were derived from the cDNAs in those clones, were used to screen the lambda gt11 library, using essentially the method described in Section IV.A.3. The probes used were:

10 5' CAG GAT GCT GTC TCC CGC ACT CAA CGT C 3'

and

5' TCC TGA GGC GAC TGC ACC AGT GGA TAA GCT 3'

15 to detect colonies containing HCV cDNA sequences which overlap those in clones 37b and 33b, respectively. Approximately 1 in 50,000 colonies were detected with each probe. A clone which contained cDNA which was upstream 20 of, and which overlapped the cDNA in clone 37b, was named clone 40b. A clone which contained cDNA which was downstream of, and which overlapped the cDNA in clone 33b was named clone 25c.

25 IV.A.15 Nucleotide Sequences of HCV cDNA in clone 40b and in clone 25c

The nucleotide sequences of the cDNAs in clone 40b and in clone 25c were determined essentially as 30 described in Section IV.A.2. The sequences of 40b and 25c, their regions of overlap with the cDNAs in clones 37b and 33b, and the putative polypeptides encoded therein, are shown in Fig. 12 (clone 40b) and Fig. 13 (clone 25c).

The 5'-terminal nucleotide of clone 40b is a G. 35 However, the cDNAs from five other independent clones

-80-

which were isolated during the procedure in which clone 40b was isolated, described in Section IV.A.14, have also been sequenced. The cDNAs from these clones also contain a T in this position. Thus, the G may represent a cloning 5 artifact (see the discussion in Section IV.A.11).

The 5'-terminus of clone 25c is ACT, but the sequence of this region in clone cla (sequence not shown), and in clone 33b is TCA. This difference may also represent a cloning artifact, as may the 28 extra 5'- 10 terminal nucleotides in clone 5-1-1.

Clones 40b and 25c each apparently contain an ORF which is an extension of the continuous ORF in the previously sequenced clones. The nucleotide sequence of the ORF extending through clones 40b, 37b, 35, 36, 81, 32, 15 33b, and 25c, and the amino acid sequence of the putative polypeptide encoded therein, are shown in Fig. 14. In the figure, the potential artifacts have been omitted from the sequence, and instead, the corresponding sequences in non- 20 5'-terminal regions of multiple overlapping clones are shown.

IV.A.16. Preparation of a Composite HCV cDNA from the cDNAs in Clones 36, 81, and 32

The composite HCV cDNA, C100, was constructed as 25 follows. First the cDNAs from the clones 36, 81, and 32 were excised with EcoRI. The EcoRI fragment of cDNA from each clone was cloned individually into the EcoRI site of the vector pGEM3-blue (Promega Biotec). The resulting recombinant vectors which contained the cDNAs from clones 30 36, 81, and 32 were named pGEM3-blue/36, pGEM3-blue/81, and pGEM3-blue/32, respectively. The appropriately oriented recombinant of pGEM3-blue/81 was digested with NaeI and NarI, and the large (~2850bp) fragment was purified and ligated with the small (~570bp) NaeI/NarI purified restriction fragment from pGEM3-blue/36. This 35

composite of the cDNAs from clones 36 and 81 was used to generate another pGEM3-blue vector containing the continuous HCV ORF contained within the overlapping cDNA within these clones. This new plasmid was then digested  
5 with PvuII and EcoRI to release a fragment of approximately 680bp, which was then ligated with the small (580bp) PvuII/EcoRI fragment isolated from the appropriately oriented pGEM3-blue/32 plasmid, and the composite cDNA from clones 36, 81, and 32 was ligated into  
10 the EcoRI linearized vector pSODcf1, which is described in Section IV.B.1, and which was used to express clone 5-1-1 in bacteria. Recombinants containing the ~1270bp EcoRI fragment of composite HCV cDNA (C100) were selected, and the cDNA from the plasmids was excised with EcoRI and  
15 purified.

IV.A.17. Isolation and Nucleotide Sequences of HCV cDNAs in Clones 14i, 11b, 7f, 7e, 8h, 33c, 14c, 8f, 33f, 33g, and 39c

20 The HCV cDNAs in clones 14i, 11b, 7f, 7e, 8h, 33c, 14c, 8f, 33f, 33g, and 39c were isolated by the technique of isolating overlapping cDNA fragments from the lambda gt11 library of HCV cDNAs described in Section IV.A.1.. The technique used was essentially as described  
25 in Section IV.A.3., except that the probes used were designed from the nucleotide sequence of the last isolated clones from the 5' and the 3' end of the combined HCV sequences. The frequency of clones which hybridized with the probes described below was approximately 1 in 50,000  
30 in each case.

The nucleotide sequences of the HCV cDNAs in clones 14i, 7f, 7e, 8h, 33c, 14c, 8f, 33f, 33g, and 39c were determined essentially as described in Section IV.A.2., except that the cDNA excised from these phages  
35 were substituted for the cDNA isolated from clone 5-1-1.

-82-

Clone 33c was isolated using a hybridization probe based on the sequence of nucleotides in clone 40b. The nucleotide sequence of clone 40b is presented in Fig. 12. The nucleotide sequence of the probe used to isolate 5 33c was:

5' ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT 3'

The sequence of the HCV cDNA in clone 33c, and the overlap 10 with that in clone 40b, is shown in Fig. 15, which also shows the amino acids encoded therein.

Clone 8h was isolated using a probe based on the sequence of nucleotides in clone 33c. The nucleotide sequence of the probe was

15 5' AGA GAC AAC CAT GAG GTC CCC GGT GTT C 3'.

The sequence of the HCV cDNA in clone 8h, and the overlap 20 with that in clone 33c, and the amino acids encoded therein, are shown in Fig. 16.

Clone 7e was isolated using a probe based on the sequence of nucleotides in clone 8h. The nucleotide sequence of the probe was

25 5' TCG GAC CTT TAC CTG GTC ACG AGG CAC 3'.

The sequence of HCV cDNA in clone 7e, the overlap with clone 8h, and the amino acids encoded therein, are shown in Fig. 17.

30 Clone 14c was isolated with a probe based on the sequence of nucleotides in clone 25c. The sequence of clone 25c is shown in Fig. 13. The probe in the isolation of clone 14c had the sequence

35 5' ACC TTC CCC ATT AAT GCC TAC ACC ACG GGC 3'.

-83-

The sequence of HCV cDNA in clone 14c, its overlap with that in clone 25c, and the amino acids encoded therein are shown in Fig. 18.

Clone 8f was isolated using a probe based on the  
5 sequence of nucleotides in clone 14c. The nucleotide sequence of the probe was

5' TCC ATC TCT CAA GGC AAC TTG CAC CGC TAA 3'.

10 The sequence of HCV cDNA in clone 8f, its overlap with that in clone 14c, and the amino acids encoded therein are shown in Fig. 19.

Clone 33f was isolated using a probe based on the nucleotide sequence present in clone 8f. The  
15 nucleotide sequence of the probe was

5' TCC ATG GCT GTC CGC TTC CAC CTC CAA AGT 3'.

20 The sequence of HCV cDNA in clone 33f, its overlap with that in clone 8f, and the amino acids encoded therein are shown in Fig. 20.

Clone 33g was isolated using a probe based on the sequence of nucleotides in clone 33f. The nucleotide sequence of the probe was

25 5' GCG ACA ATA CGA CAA CAT CCT CTG AGC CCG 3'.

The sequence of HCV cDNA in clone 33g, its overlap with that in clone 33f, and the amino acids encoded therein are  
30 shown in Fig. 21.

Clone 7f was isolated using a probe based on the sequence of nucleotides in clone 7e. The nucleotide sequence of the probe was

35 5' AGC AGA CAA GGG GCC TCC TAG GGT GCA TAA T 3'.

-84-

The sequence of HCV cDNA in clone 7f, its overlap with clone 7e, and the amino acids encoded therein are shown in Fig. 22.

Clone 11b was isolated using a probe based on  
5 the sequence of clone 7f. The nucleotide sequence of the probe was

5' CAC CTA TGT TTA TAA CCA TCT CAC TCC TCT 3'.

10 The sequence of HCV cDNA in clone 11b, its overlap with clone 7f, and the amino acids encoded therein are shown in Fig. 23.

Clone 14i was isolated using a probe based on  
the sequence of nucleotides in clone 11b. The nucleotide  
15 sequence of the probe was

5' CTC TGT CAC CAT ATT ACA AGC GCT ATA TCA 3'.

20 The sequence of HCV cDNA in clone 14i, its overlap with  
clone 11b, and the amino acids encoded therein are shown in Fig.  
24.

Clone 39c was isolated using a probe based on  
the sequence of nucleotides in clone 33g. The nucleotide  
sequence of the probe was

25 5' CTC GTT GCT ACG TCA CCA CAA TTT GGT GTA 3'

30 The sequence of HCV cDNA in clone 39c, its overlap with  
clone 33g, and the amino acids encoded therein are shown  
in Fig. 25.

IV.A.18. The Composite HCV cDNA Sequence Derived from  
Isolated Clones Containing HCV cDNA

35 The HCV cDNA sequences in the isolated clones described supra have been aligned to create a composite

HCV cDNA sequence. The isolated clones, aligned in the 5' to 3' direction are: 14i, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g, and 39c.

5 A composite HCV cDNA sequence derived from the isolated clones, and the amino acids encoded therein, is shown in Fig. 26.

In creating the composite sequence the following sequence heterogeneities have been considered. Clone 33c contains an HCV cDNA of 800 base pairs, which overlaps the 10 cDNAs in clones 40b and 37c. In clone 33c, as well as in 5 other overlapping clones, nucleotide #789 is a G. However, in clone 37b (see Section IV.A.11), the corresponding nucleotide is an A. This sequence difference creates an apparent heterogeneity in the amino acids 15 encoded therein, which would be either CYS or TYR, for G or A, respectively. This heterogeneity may have important ramifications in terms of protein folding.

Nucleotide residue #2 in clone 8h HCV cDNA is a T. However, as shown infra, the corresponding residue in 20 clone 7e is an A; moreover, an A in this position is also found in 3 other isolated overlapping clones. Thus, the T residue in clone 8h may represent a cloning artifact. Therefore, in Fig. 26, the residue in this position is designated as an A.

25 The 3'-terminal nucleotide in clone 8f HCV cDNA is a G. However, the corresponding residue in clone 33f, and in 2 other overlapping clones is a T. Therefore, in Fig. 26, the residue in this position is designated as a T.

30 The 3'-terminal sequence in clone 33f HCV cDNA is TTGC. However, the corresponding sequence in clone 33g and in 2 other overlapping clones is ATTC. Therefore, in Fig. 26, the corresponding region is represented as ATTC.

35 Nucleotide residue #4 in clone 33g HCV cDNA is a T. However, in clone 33f and in 2 other overlapping

-86-

clones the corresponding residue is an A. Therefore, in Fig. 26, the corresponding residue is designated as an A.

The 3'-terminus of clone 14i is an AA, whereas the corresponding dinucleotide in clone 11b, and in three 5 other clones, is TA. Therefore, in Fig. 26, the TA residue is depicted.

The resolution of other sequence heterogeneities is discussed supra.

An examination of the composite HCV cDNA 10 indicates that it contains one large ORF. This suggests that the viral genome is translated into a large polypeptide which is processed concomitant with, or subsequent to translation.

15 IV.A.19. Isolation and Nucleotide Sequences of HCV cDNAs in Clones 12f, 35f, 19g, 26g, and 15e

The HCV cDNAs in clones 12f, 35f, 19g, 26g, and 15e were isolated essentially by the technique described in Section IV.A.17, except that the probes were as 20 indicated below. The frequency of clones which hybridized with the probes was approximately 1 in 50,000 in each case. The nucleotide sequences of the HCV cDNAs in these clones were determined essentially as described in Section IV.A.2., except that the cDNA from the indicated clones 25 were substituted for the cDNA isolated from clone 5-1-1.

The isolation of clone 12f, which contains cDNA upstream of the HCV cDNA in Fig. 26, was accomplished using a hybridization probe based on the sequence of nucleotides in clone 14i. The nucleotide sequence of the 30 probe was

5' TGC TTG TGG ATG ATG CTA CTC ATA TCC CAA 3'.

-87-

The HCV cDNA sequence of clone 12f, its overlap with clone 14i, and the amino acids encoded therein are shown in Fig. 27.

\* 5 The isolation of clone 35f, which contains cDNA downstream of the HCV cDNA in Fig. 26, was accomplished using a hybridization probe based on the sequence of nucleotides in clone 39c. The nucleotide sequence of the probe was

10 5' AGC AGC GGC GTC AAA AGT GAA GGC TAA CTT 3'.

The sequence of clone 35f, its overlap with the sequence in clone 39c, and the amino acids encoded therein are shown in Fig. 28.

15 The isolation of clone 19g was accomplished using a hybridization probe based on the 3' sequence of clone 35f. The nucleotide sequence of the probe was

5' TTC TCG TAT GAT ACC CGC TGC TTT GAC TCC 3'.

20 The HCV cDNA sequence of clone 19g, its overlap with the sequence in clone 35f, and the amino acids encoded therein are shown in Fig. 29.

25 The isolation of clone 26g was accomplished using a hybridization probe based on the 3' sequence of clone 19g. The nucleotide sequence of the probe was

5' TGT GTG GCG ACG ACT TAG TCG TTA TCT GTG 3'.

30 The HCV cDNA sequence of clone 26g, its overlap with the sequence in clone 19g, and the amino acids encoded therein are shown in Fig. 30.

\* Clone 15e was isolated using a hybridization probe based on the 3' sequence of clone 26 g. The 35 nucleotide sequence of the probe was

-88-

5' CAC ACT CCA GTC AAT TCC TGG CTA GGC AAC 3'.

The HCV cDNA sequence of clone 15e, its overlap with the sequence in clone 26g, and the amino acids encoded therein  
5 are shown in Fig. 31.

The clones described in this Section have been deposited with the ATCC under the terms and conditions described in Section II.A., and have been assigned the following Accession Numbers.

10

	<u>lambda-gt11</u>	<u>ATCC No.</u>	<u>Deposit Date</u>
	clone 12f	40514	10 Nov. 1988
	clone 35f	40511	10 Nov. 1988
	clone 15e	40513	10 Nov. 1988
15	clone K9-1	40512	10 Nov. 1988

The HCV cDNA sequences in the isolated clones described supra. have been aligned to create a composite HCV cDNA sequence. The isolated clones, aligned in the 5'  
20 to 3' direction are: 12f, 14i, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f 33f, 33g, 39c, 35f, 19g, 26g, and 15e.

A composite HCV cDNA sequence derived from the isolated clones, and the amino acids encoded therein, is  
25 shown in Fig. 32.

IV.A.20. Alternative Method of Isolating cDNA Sequences Upstream of the HCV cDNA Sequence in Clone 12f

Based on the most 5' HCV sequence in Fig. 32,  
30 which is derived from the HCV cDNA in clone 12f, small synthetic oligonucleotide primers of reverse transcriptase are synthesized and used to bind to the corresponding sequence in HCV genomic RNA, to prime reverse transcription of the upstream sequences. The primer

35

sequences are proximal to the known 5'-terminal sequence of clone 12f, but sufficiently downstream to allow the design of probe sequences upstream of the primer sequences. Known standard methods of priming and cloning  
5 are used. The resulting cDNA libraries are screened with sequences upstream of the priming sites (as deduced from the elucidated sequence in clone 12f). The HCV genomic RNA is obtained from either plasma or liver samples from chimpanzees with NANBH, or from analogous samples from  
10 humans with NANBH.

IV.A.21. Alternative Method Utilizing Tailing to Isolate Sequences from the 5'-Terminal Region of the HCV Genome

In order to isolate the extreme 5'-terminal sequences of the HCV RNA genome, the cDNA product of the first round of reverse transcription, which is duplexed with the template RNA, is tailed with oligo C. This is accomplished by incubating the product with terminal transferase in the presence of CTP. The second round of  
15 cDNA synthesis, which yields the complement of the first strand of cDNA, is accomplished utilizing oligo G as a primer for the reverse transcriptase reaction. The sources of genomic HCV RNA are as described in Section  
20 IV.A.20. The methods for tailing with terminal transferase, and for the reverse transcriptase reactions are as in Maniatis et al. (1982). The cDNA products are  
25 then cloned, screened, and sequenced.

IV.A.22. Alternative Method Utilizing Tailing to Isolate Sequences from the 3'-Terminal Region of the HCV Genome

This method is based on previously used methods for cloning cDNAs of Flavivirus RNA. In this method, the RNA is subjected to denaturing conditions to remove secondary structures at the 3'-terminus, and is then  
35 tailed with Poly A polymerase using rATP as a substrate.

-90-

Reverse transcription of the poly A tailed RNA is catalyzed by reverse transcriptase, utilizing oligo dT as a primer. The second strands of cDNA are synthesized, the cDNA products are cloned, screened, and sequenced.

5

IV.A.23 Creation of Lambda-gt11 HCV cDNA Libraries Containing Larger cDNA Inserts

The method used to create and screen the Lambda gt11 libraries are essentially as described in Section 10 IV.A.1., except that the library is generated from a pool of larger size cDNAs eluted from the Sepharose CL-4B column.

IV.A.24. Creation of HCV cDNA Libraries Using Synthetic Oligomers as Primers

New HCV cDNA libraries have been prepared from the RNA derived from the infectious chimpanzee plasma pool described in Section IV.A.1., and from the poly A<sup>+</sup> RNA fraction derived from the liver of this infected animal.

20 The cDNA was constructed essentially as described by Gubler and Hoffman (1983), except that the primers for the first cDNA strand synthesis were two synthetic oligomers based on the sequence of the HCV genome described supra. Primers based on the sequence of clone 11 b and 7e were, 25 respectively,

5' CTG GCT TGA AGA ATC 3'

and

30

5' AGT TAG GCT GGT GAT TAT GC 3'.

The resulting cDNAs were cloned into lambda bacteriophage vectors, and screened with various other synthetic

35

oligomers, whose sequences were based on the HCV sequence in Fig. 32.

IV.B. Expression of Polypeptides Encoded Within HCV cDNAs  
5 and Identification of the Expressed Products as HCV  
Induced Antigens.

**IV.B.1. Expression of the Polypeptide Encoded in Clone 5-1-1.**

10 The HCV polypeptide encoded within clone 5-1-1  
(see Section IV.A.2., supra) was expressed as a fusion  
polypeptide with superoxide dismutase (SOD). This was  
accomplished by subcloning the clone 5-1-1 cDNA insert  
into the expression vector pSODcfl (Steimer et al. (1986))  
15 as follows.

First, DNA isolated from pSODcfl was treated with BamHI and EcoRI, and the following linker was ligated into the linear DNA created by the restriction enzymes:

20                    5' GAT CCT GGA ATT CTG ATA A                    3'  
                       3'                    GA CCT TAA GAC TAT TTT AA                    5'

After cloning, the plasmid containing the insert was isolated.

25 Plasmid containing the insert was restricted  
with EcoRI. The HCV cDNA insert in clone 5-1-1 was  
excised with EcoRI, and ligated into this EcoRI linearized  
plasmid DNA. The DNA mixture was used to transform E.  
coli strain D1210 (Sadler et al. (1980)). Recombinants  
30 with the 5-1-1 cDNA in the correct orientation for  
expression of the ORF shown in Fig. 1 were identified by  
restriction mapping and nucleotide sequencing.

Recombinant bacteria from one clone were induced to express the SOD-NANB<sub>5-1-1</sub> polypeptide by growing the bacteria in the presence of IPTG.

-92-

IV.B.2. Expression of the Polypeptide Encoded in Clone 81.

The HCV cDNA contained within clone 81 was expressed as a SOD-NANB<sub>81</sub> fusion polypeptide. The method 5 for preparing the vector encoding this fusion polypeptide was analogous to that used for the creation of the vector encoding SOD-NANB<sub>5-1-1</sub>, except that the source of the HCV cDNA was clone 81, which was isolated as described in Section IV.A.3, and for which the cDNA sequence was 10 determined as described in Section IV.A.4. The nucleotide sequence of the HCV cDNA in clone 81, and the putative amino acid sequence of the polypeptide encoded therein are shown in Fig. 4.

The HCV cDNA insert in clone 81 was excised with 15 EcoRI, and ligated into the pSODcf1 which contained the linker (see IV.B.1.) and which was linearized by treatment with EcoRI. The DNA mixture was used to transform E. coli strain D1210. Recombinants with the clone 81 HCV cDNA in the correct orientation for expression of the ORF shown in 20 Fig. 4 were identified by restriction mapping and nucleotide sequencing.

Recombinant bacteria from one clone were induced to express the SOD-NANB<sub>81</sub> polypeptide by growing the bacteria in the presence of IPTG.

25  
IV.B.3. Identification of the Polypeptide Encoded Within Clone 5-1-1 as an HCV and NANBH Associated Antigen.

The polypeptide encoded within the HCV cDNA of clone 5-1-1 was identified as a NANBH associated antigen 30 by demonstrating that sera of chimpanzees and humans infected with NANBH reacted immunologically with the fusion polypeptide, SOD-NANB<sub>5-1-1</sub>, which is comprised of superoxide dismutase at its N-terminus and the in-frame 5-1-1 antigen at its C-terminus. This was accomplished by 35 "Western" blotting (Towbin et al. (1979)) as follows.

A recombinant strain of bacteria transformed with an expression vector encoding the SOD-NANB<sub>5-1-1</sub> polypeptide, described in Section IV.B.I., was induced to express the fusion polypeptide by growth in the presence 5 of IPTG. Total bacterial lysate was subjected to electrophoresis through polyacrylamide gels in the presence of SDS according to Laemmli (1970). The separated polypeptides were transferred onto nitrocellulose filters (Towbin et al. (1979)). The filters were then cut into 10 thin strips, and the strips were incubated individually with the different chimpanzee and human sera. Bound antibodies were detected by further incubation with <sup>125</sup>I-labeled sheep anti-human Ig, as described in Section IV.A.1.

15 The characterization of the chimpanzee sera used for the Western blots and the results, shown in the photograph of the autoradiographed strips, are presented in Fig. 33. Nitrocellulose strips containing polypeptides were incubated with sera derived from chimpanzees at different times during acute NANBH (Hutchinson strain) infections (lanes 1-16), hepatitis A infections (lanes 17-24, and 26-33), and hepatitis B infections (lanes 34-44). Lanes 25 and 45 show positive controls in which the 20 immunoblots were incubated with serum from the patient used to identify the recombinant clone 5-1-1 in the 25 original screening of the lambda-gt11 cDNA library (see Section IV.A.1.).

The band visible in the control lanes, 25 and 45, in Fig. 23 reflects the binding of antibodies to the 30 NANB<sub>5-1-1</sub> moiety of the SOD fusion polypeptide. These antibodies do not exhibit binding to SOD alone, since this has also been included as a negative control in these samples, and would have appeared as a band migrating significantly faster than the SOD-NANB<sub>5-1-1</sub> fusion 35 polypeptide.

Lanes 1-16 of Fig. 33 show the binding of anti-bodies in sera samples of 4 chimpanzees; the sera were obtained just prior to infection with NANBH, and sequentially during acute infection. As seen from the 5 figure, whereas antibodies which reacted immunologically with the SOD-NANB<sub>5-1-1</sub> polypeptide were absent in sera samples obtained before administration of infectious HCV inoculum and during the early acute phase of infection, all 4 animals eventually induced circulating antibodies to 10 this polypeptide during the late part of, or following the acute phase. Additional bands observed on the immunoblots in the cases of chimps numbers 3 and 4 were due to background binding to host bacterial proteins.

In contrast to the results obtained with sera 15 from chimps infected with NANBH, the development of anti-bodies to the NANB<sub>5-1-1</sub> moiety of the fusion polypeptide was not observed in 4 chimpanzees infected with HAV or 3 chimpanzees infected with HBV. The only binding in these 20 cases was background binding to the host bacterial proteins, which also occurred in the HCV infected samples.

The characterization of the human sera used for the Western blots, and the results, which are shown in the photograph of the autoradiographed strips, are presented in Fig. 34. Nitrocellulose strips containing polypeptides 25 were incubated with sera derived from humans at different times during infections with NANBH (lanes 1-21), HAV (lanes 33-40), and HBV (lanes 41-49). Lanes 25 and 50 show positive controls in which the immunoblots were incubated with serum from patient used in the original 30 screening of the lambda-gt11 library, described supra. Lanes 22-24 and 26-32 show "non-infected" controls in which the sera was from "normal" blood donors.

As seen in Fig. 34, sera from nine NANBH patients, including the serum used for screening the 35 lambda-gt11 library, contained antibodies to the NANB<sub>5-1-1</sub>

moiety of the fusion polypeptide. Sera from three patients with NANBH did not contain these antibodies. It is possible that the anti-NANB<sub>5-1-1</sub> antibodies will develop at a future date in these patients. It is also 5 possible that this lack of reaction resulted from a different NANBV agent being causative of the disease in the individuals from which the non-responding serum was taken.

Fig. 34 also shows that sera from many patients infected with HAV and HBV did not contain anti-NANB<sub>5-1-1</sub> 10 antibodies, and that these antibodies were also not present in the sera from "normal" controls. Although one HAV patient (lane 36) appears to contain anti-NANB<sub>5-1-1</sub> antibodies, it is possible that this patient had been previously infected with HCV, since the incidence of NANBH 15 is very high and since it is often subclinical.

These serological studies indicate that the cDNA in clone 5-1-1 encodes epitopes which are recognized specifically by sera from patients and animals infected with BB-NANBV. In addition, the cDNA does not appear to 20 be derived from the primate genome. A hybridization probe made from clone 5-1-1 or from clone 81 did not hybridize to "Southern" blots of control human and chimpanzee genomic DNA from uninfected individuals under conditions where unique, single-copy genes are detectable. These 25 probes also did not hybridize to Southern blots of control bovine genomic DNA.

#### IV.B.4. Expression of the Polypeptide Encoded in a Composite of the HCV cDNAs in Clones 36, 81 and 32

30 The HCV polypeptide which is encoded in the ORF which extends through clones 36, 81 and 32 was expressed as a fusion polypeptide with SOD. This was accomplished by inserting the composite cDNA, C100, into an expression cassette which contains the human superoxide dismutase 35 gene, inserting the expression cassette into a yeast

-96-

expression vector, and expressing the polypeptide in yeast.

An expression cassette containing the composite C100 cDNA derived from clones 36, 81, and 32, was 5 constructed by inserting the ~1270bp EcoRI fragment into the EcoRI site of the vector pS3-56 (also called pS356), yielding the plasmid pS3-56<sub>C100</sub>. The construction of C100 is described in Section IV.A.16, supra.

The vector pS3-56, which is a pBR322 derivative, 10 contains an expression cassette which is comprised of the ADH2/GAPDH hybrid yeast promoter upstream of the human superoxide dismutase gene, and a downstream GAPDH transcription terminator. A similar cassette, which contains these control elements and the superoxide 15 dismutase gene has been described in Cousens et al. (1987), and in copending application EPO 196,056, published October 1, 1986, which is commonly owned by the herein assignee. The cassette in pS3-56, however, differs from that in Cousens et al. (1987) in that the 20 heterologous proinsulin gene and the immunoglobulin hinge are deleted, and in that the gln<sub>154</sub> of the superoxide dismutase is followed by an adaptor sequence which contains an EcoRI site. The sequence of the adaptor is:

25           5'-AAT TTG GGA ATT CCA TAA TGA G       -3'  
                AC CCT TAA GGT ATT ACT CAG CT .

The EcoRI site allows the insertion of heterologous sequences which, when expressed from a vector containing 30 the cassette, yield polypeptides which are fused to superoxide dismutase via an oligopeptide linker containing the amino acid sequence:

-asn-leu-gly-ile-arg-.

A sample of pS356 has been deposited on 29 April 1988 under the terms of the Budapest Treaty with the American Type Culture Collection (ATCC), 12301 Parklawn Dr., Rockville, Maryland 20853, and has been assigned Accession No. 67683. The terms and conditions for availability and access to the deposit, and for maintenance of the deposit are the same as those specified in Section II.A., for strains containing NANBV-cDNAs. This deposit is intended for convenience only, and is not required to practice the present invention in view of the description here. The deposited material is hereby incorporated herein by reference.

After recombinants containing the C100 cDNA insert in the correct orientation were isolated, the expression cassette containing the C100 cDNA was excised from pS3-56<sub>C100</sub> with BamHI, and a fragment of ~3400bp which contains the cassette was isolated and purified. This fragment was then inserted into the BamHI site of the yeast vector pAB24.

Plasmid pAB24, the significant features of which are shown in Fig. 35, is a yeast shuttle vector which contains the complete 2 micron sequence for replication [Broach (1981)] and pBR322 sequences. It also contains the yeast URA3 gene derived from plasmid YEp24 [Botstein et al. (1979)], and the yeast LEU<sup>2d</sup> gene derived from plasmid pC1/1. EPO Pub. No. 116,201. Plasmid pAB24 was constructed by digesting YEp24 with EcoRI and religating the vector to remove the partial 2 micron sequences. The resulting plasmid, YEP24deltaRI, was linearized by digestion with Clal and ligated with the complete 2 micron plasmid which had been linearized with Clal. The resulting plasmid, pCBou, was then digested with XbaI and the 8605 bp vector fragment was gel isolated. This isolated XbaI fragment was ligated with a 4460 bp XbaI fragment containing the LEU<sup>2d</sup> gene isolated from pC1/1;

the orientation of the LEU<sup>2d</sup> gene is in the same direction as the URA3 gene. Insertion of the expression was in the unique BamHI site of the pBR322 sequence, thus interrupting the gene for bacterial resistance to  
5 tetracycline.

The recombinant plasmid which contained the SOD-C100 expression cassette, pAB24C100-3, was transformed into yeast strain JSC 308, as well as into other yeast strains. The cells were transformed as described by  
10 Hinnen et al. (1978), and plated onto ura-selective plates. Single colonies were inoculated into leu-selective media and grown to saturation. The culture was induced to express the SOD-C100 polypeptide (called C100-3) by growth in YEP containing 1% glucose.

Strain JSC 308 is of the genotype MAT  $\alpha$ , leu2, ura3(del) DM15 (GAP/ADR1) integrated at the ADR1 locus. In JSC 308, over-expression of the positive activator gene product, ADR1, results in hyperderepression (relative to an ADR1 wild type control) and significantly higher yields  
20 of expressed heterologous proteins when such proteins are synthesized via an ADH2 UAS regulatory system. The construction of the yeast strain JSC 308 is disclosed in copending application, U.S. Serial No. (Attorney Docket No. 2300-0229), filed concurrently herewith, and which is  
25 hereby incorporated herein by reference. A sample of JSC 308 has been deposited on 5 May 1988 with the ATCC under the conditions of the Budapest Treaty, and has been assigned Accession No. 20879. The terms and conditions for availability and access to the deposit, and for  
30 maintenance of the deposit are the same as those specified in Section II.A., for strains containing HCV cDNAs.

The complete C100-3 fusion polypeptide encoded in pAB24C100-3 should contain 154 amino acids of human SOD at the amino-terminus, 5 amino acid residues derived from  
35 the synthetic adaptor containing the EcoRI site, 363 amino

acid residues derived from C100 cDNA, and 5 carboxy-terminal amino acids derived from the MS2 nucleotide sequence adjoining the HCV cDNA sequence in clone 32.

(See Section IV.A.7.) The putative amino acid sequence of 5 the carboxy-terminus of this polypeptide, beginning at the penultimate Ala residue of SOD, is shown in Fig. 36; also shown is the nucleotide sequence encoding this portion of the polypeptide.

10 **IV.B.5. Identification of the Polypeptide Encoded within C100 as an NANBH Associated Antigen**

The C100-3 fusion polypeptide expressed from plasmid pAB24C100-3 in yeast strain JSC 308 was characterized with respect to size, and the polypeptide encoded 15 within C100 was identified as an NANBH-associated antigen by its immunological reactivity with serum from a human with chronic NANBH.

The C100-3 polypeptide, which was expressed as described in Section IV.B.4., was analyzed as follows. 20 Yeast JSC 308 cells were transformed with pAB24, or with pAB24C100-3, and were induced to express the heterologous plasmid encoded polypeptide. The induced yeast cells in 1 ml of culture ( $OD_{650\text{ nm}} \sim 20$ ) were pelleted by centrifugation at 10,000 rpm for 1 minute, and were lysed 25 by vortexing them vigorously (10 x 1 min) with 2 volumes of solution and 1 volume of glass beads (0.2 millimicron diameter). The solution contained 50 mM Tris-HCl, pH 8.0, 1 mM EDTA, 1mM phenylmethylsulphonyl fluoride (PMSF), and 1 microgram/ml pepstatin. Insoluble material in the 30 lysate, which includes the C100-3 polypeptide, was collected by centrifugation (10,000 rpm for 5 minutes), and was dissolved by boiling for 5 minutes in Laemmli SDS sample buffer. [See Laemmli (1970)]. An amount of 35 polypeptides equivalent to that in 0.3 ml of the induced yeast culture was subjected to electrophoresis through 10%

-100-

polyacrylamide gels in the presence of SDS according to Laemmli (1970). Protein standards were co-electrophoresed on the gels. Gels containing the expressed polypeptides were either stained with Coomassie brilliant blue, or were 5 subjected to "Western" blotting as described in Section IV.B.2., using serum from a patient with chronic NANBH to determine the immunological reactivity of the polypeptides expressed from pAB24 and from pAB24C100-3.

The results are shown in Fig. 37. In Fig. 37A 10 the polypeptides were stained with Coomassie brilliant blue. The insoluble polypeptide(s) from JSC 308 transformed with pAB24 and from two different colonies of JSC transformed with pAB24C100-3 are shown in lane 1 (pAB24), and lanes 2 and 3, respectively. A comparison of lanes 2 15 and 3 with lane 1 shows the induced expression of a polypeptide corresponding to a molecular weight of ~54,000 daltons from JSC 308 transformed with pAB24C100-3, which is not induced in JSC 308 transformed with pAB24. This polypeptide is indicated by the arrow.

Fig. 37B shows the results of the Western blots 20 of the insoluble polypeptides expressed in JSC 308 transformed with pAB24 (lane 1), or with pAB24C100-3 (lane 2). The polypeptides expressed from pAB24 were not immunologically reactive with serum from a human with NANBH. 25 However, as indicated by the arrow, JSC 308 transformed with pAB24C100-3 expressed a polypeptide of ~54,000 dalton molecular weight which did react immunologically with the human NANBH serum. The other immunologically reactive polypeptides in lane 2 may be degradation and/or aggregation 30 products of this ~54,000 dalton polypeptide.

#### IV.B.6. Purification of Fusion Polypeptide C100-3

The fusion polypeptide, C100-3, comprised of SOD at the N-terminus and in-frame C100 HCV-polypeptide at the 35 C-terminus was purified by differential extraction of the

insoluble fraction of the extracted host yeast cells in which the polypeptide was expressed.

The fusion polypeptide, C100-3, was expressed in yeast strain JSC 308 transformed with pAB24C100-3, as 5 described in Section IV.B.4. The yeast cells were then lysed by homogenization, the insoluble material in the lysate was extracted at pH 12.0, and C100-3 in the remaining insoluble fraction was solubilized in buffer containing SDS.

10 The yeast lysate was prepared essentially according to Nagahuma et al. (1984). A yeast cell suspension was prepared which was 33% cells (v/v) suspended in a solution (Buffer A) containing 20 mM Tris HCl, pH 8.0, 1 mM dithiothreitol, and 1 mM phenylmethylsulfonylfluoride 15 (PMSF). An aliquot of the suspension (15 ml) was mixed with an equal volume of glass beads (0.45-0.50 mm diameter), and the mixture was vortexed at top speed on a Super Mixer (Lab Line Instruments, Inc.) for 8 min. The homogenate and glass beads were separated, and the glass 20 beads were washed 3 times with the same volume of Buffer A as the original packed cells. After combining the washes and homogenate, the insoluble material in the lysate was obtained by centrifuging the homogenate at 7,000 x g for 15 minutes at 4°C, resuspending the pellets in Buffer A 25 equal to twice the volume of original packed cells, and re-pelleting the material by centrifugation at 7,000 x g for 15 min. This washing procedure was repeated 3 times.

The insoluble material from the lysate was extracted at pH 12.0 as follows. The pellet was suspended 30 in buffer containing 0.5 M NaCl, 1 mM EDTA, where the suspending volume was equal to 1.8 times the of the original packed cells. The pH of the suspension was adjusted by adding 0.2 volumes of 0.4 M Na phosphate buffer, pH 12.0. After mixing, the suspension was 35 centrifuged at 7,000 x g for 15 min at 4°C, and the super-

natant removed. The extraction was repeated 2 times. The extracted pellets were washed by suspending them in 0.5 M NaCl, 1 mM EDTA, using a suspension volume equal to two volumes of the original packed cells, followed by 5 centrifugation at 7,000 x g for 15 min at 4°C.

The C100-3 polypeptide in the extracted pellet was solubilized by treatment with SDS. The pellets were suspended in Buffer A equal to 0.9 volumes of the original packed cell volume, and 0.1 volumes of 2% SDS was added.

10 After the suspension was mixed, it was centrifuged at 7,000 x g for 15 min at 4°C. The resulting pellet was extracted 3 more times with SDS. The resulting supernatants, which contained C100-3 were pooled.

15 This procedure purifies C100-3 more than 10-fold from the insoluble fraction of the yeast homogenate, and the recovery of the polypeptide is greater than 50%.

20 The purified preparation of fusion polypeptide was analyzed by polyacrylamide gel electrophoresis according to Laemmli (1970). Based upon this analysis, the polypeptide was greater than 80% pure, and had an apparent molecular weight of ~54,000 daltons.

#### IV.C. Identification of RNA in Infected Individuals Which Hybridizes to HCV cDNA.

25 IV.C.1. Identification of RNA in the Liver of a Chimpanzee With NANBH Which Hybridizes to HCV cDNA.

RNA from the liver of a chimpanzee which had NANBH was shown to contain a species of RNA which hybridized to the HCV cDNA contained within clone 81 by Northern blotting, as follows.

RNA was isolated from a liver biopsy of the chimpanzee from which the high titer plasma was derived (see Section IV.A.1.) using techniques described in 35 Maniatis et al. (1982) for the isolation of total RNA from

mammalian cells, and for its separation into poly A<sup>+</sup> and poly A<sup>-</sup> fractions. These RNA fractions were subjected to electrophoresis on a formaldehyde/agarose gel (1% w/v), and transferred to nitrocellulose. (Maniatis et al. 5 (1982)). The nitrocellulose filters were hybridized with radiolabeled HCV cDNA from clone 81 (see Fig. 4 for the nucleotide sequence of the insert.) To prepare the radiolabeled probe, the HCV cDNA insert isolated from clone 81 was radiolabeled with <sup>32</sup>P by nick translation 10 using DNA Polymerase I (Maniatis et al. (1982)). Hybridization was for 18 hours at 42°C in a solution containing 10% (w/v) Dextran sulphate, 50% (w/v) deionized formamide, 750 mM NaCl, 75 mM Na citrate, 20 mM Na<sub>2</sub>HPO<sub>4</sub>, pH 6.5, 0.1% SDS, 0.02% (w/v) bovine serum albumin (BSA), 15 0.02% (w/v) Ficoll-400, 0.02% (w/v) polyvinylpyrrolidone, 100 micrograms/ml salmon sperm DNA which had been sheared by sonication and denatured, and 10<sup>6</sup> CPM/ml of the nick-translated cDNA probe.

An autoradiograph of the probed filter is shown 20 in Fig. 38. Lane 1 contains <sup>32</sup>P-labeled restriction fragment markers. Lanes 2-4 contain chimpanzee liver RNA as follows: lane 2 contains 30 micrograms of total RNA; lane 3 contains 30 micrograms of poly A- RNA; and lane 4 contains 20 micrograms of poly A+ RNA. As shown in Fig. 25 38, the liver of the chimpanzee with NANBH contains a heterogeneous population of related poly A+ RNA molecules which hybridizes to the HCV cDNA probe, and which appears to be from about 5000 nucleotides to about 11,000 30 nucleotides in size. This RNA, which hybridizes to the HCV cDNA, could represent viral genomes and/or specific transcripts of the viral genome.

The experiment described in Section IV.C.2., infra, is consistent with the suggestion that HCV contains an RNA genome.

-104-

IV.C.2. Identification of HCV Derived RNA in Serum from Infected Individuals.

Nucleic acids were extracted from particles isolated from high titer chimpanzee NANBH plasma as described in Section IV.A.1.. Aliquots (equivalent to 1 ml of original plasma) of the isolated nucleic acids were resuspended in 20 microliters 50 mM Hepes, pH 7.5, 1 mM EDTA and 16 micrograms/ml yeast soluble RNA. The samples were denatured by boiling for 5 minutes followed by immediate freezing, and were treated with RNase A (5 microliters containing 0.1 mg/ml RNase A in 25 mM EDTA, 40 mM Hepes, pH 7.5) or with DNase I (5 microliters containing 1 unit DNase I in 10 mM MgCl<sub>2</sub>, 25 mM Hepes, pH 7.5); control samples were incubated without enzyme. Following incubation, 230 microliters of ice-cold 2XSSC containing 2 micrograms/ml yeast soluble RNA was added, and the samples were filtered on a nitrocellulose filter. The filters were hybridized with a cDNA probe from clone 81, which had been <sup>32</sup>P-labeled by nick-translation. Fig. 39 shows an autoradiograph of the filter. Hybridization signals were detected in the DNase treated and control samples (lanes 2 and 1, respectively), but were not detected in the RNase treated sample (lane 3). Thus, since RNase A treatment destroyed the nucleic acids isolated from the particles, and DNase I treatment had no effect, the evidence strongly suggests that the HCV genome is composed of RNA.

IV.C.3. Detection of Amplified HCV Nucleic Acid Sequences derived from HCV Nucleic Acid Sequences in Liver and Plasma Specimens from Chimpanzees with NANBH

HCV nucleic acids present in liver and plasma of chimpanzees with NANBH, and in control chimpanzees, were amplified using essentially the polymerase chain reaction (PCR) technique described by Saiki et al. (1986). The primer oligonucleotides were derived from the HCV cDNA

sequences in clone 81, or clones 36 and 37. The amplified sequences were detected by gel electrophoresis and Southern blotting, using as probes the appropriate cDNA oligomer with a sequence from the region between, but not including, the two primers.

Samples of RNA containing HCV sequences to be examined by the amplification system were isolated from liver biopsies of three chimpanzees with NANBH, and from two control chimpanzees. The isolation of the RNA fraction was by the guanidinium thiocyanate procedure described in Section IV.C.1.

Samples of RNA which were to be examined by the amplification system were also isolated from the plasmas of two chimpanzees with NANBH, and from one control chimpanzee, as well as from a pool of plasmas from control chimpanzees. One infected chimpanzee had a CID/ml equal to or greater than  $10^6$ , and the other infected chimpanzee had a CID/ml equal to or greater than  $10^5$ .

The nucleic acids were extracted from the plasma as follows. Either 0.1 ml or 0.01 ml of plasma was diluted to a final volume of 1.0 ml, with a TENB/proteinase K/SDS solution (0.05 M Tris-HCl, pH 8.0, 0.001 M EDTA, 0.1 M NaCl, 1 mg/ml Proteinase K, and 0.5% SDS) containing 10 micrograms/ml polyadenylic acid, and incubated at 37°C for 60 minutes. After this proteinase K digestion, the resultant plasma fractions were deproteinized by extraction with TE (10.0 mM Tris-HCl, pH 8.0, 1 mM EDTA) saturated phenol. The phenol phase was separated by centrifugation, and was reextracted with TENB containing 0.1% SDS. The resulting aqueous phases from each extraction were pooled, and extracted twice with an equal volume of phenol/chloroform/isoamyl alcohol [1:1(99:2)], and then twice with an equal volume of a 99:1 mixture of chloroform/isoamyl alcohol. Following phase separation by centrifugation, the aqueous phase was

-106-

brought to a final concentration of 0.2 M Na Acetate, and the nucleic acids were precipitated by the addition of two volumes of ethanol. The precipitated nucleic acids were recovered by ultracentrifugation in a SW 41 rotor at 38 K,  
5 for 60 minutes at 4°C.

In addition to the above, the high titer chimpanzee plasma and the pooled control plasma alternatively were extracted with 50 micrograms of poly A carrier by the procedure of Chomczynski and Sacchi (1987).  
10 This procedure uses an acid guanidinium thiocyanate extraction. RNA was recovered by centrifugation at 10,000 RPM for 10 minutes at 4°C in an Eppendorf microfuge.

On two occasions, prior to the synthesis of cDNA in the PCR reaction, the nucleic acids extracted from  
15 plasma by the proteinase K/SDS/phenol method were further purified by binding to and elution from S and S Elutip-R Columns. The procedure followed was according to the manufacturer's directions.

The cDNA used as a template for the PCR reaction  
20 was derived from the nucleic acids (either total nucleic acids or RNA) prepared as described above. Following ethanol precipitation, the precipitated nucleic acids were dried, and resuspended in DEPC treated distilled water. Secondary structures in the nucleic acids were disrupted  
25 by heating at 65°C for 10 minutes, and the samples were immediately cooled on ice. cDNA was synthesized using 1 to 3 micrograms of total chimpanzee RNA from liver, or from nucleic acids (or RNA) extracted from 10 to 100 microliters of plasma. The synthesis utilized reverse  
30 transcriptase, and was in a 25 microliter reaction, using the protocol specified by the manufacturer, BRL. The primers for cDNA synthesis were those also utilized in the PCR reaction, described below. All reaction mixtures for cDNA synthesis contained 23 units of the RNAase inhibitor,  
35 RNasin™ (Fisher/Promega). Following cDNA synthesis, the

reaction mixtures were diluted with water, boiled for 10 minutes, and quickly chilled on ice.

The PCR reactions were performed essentially according to the manufacturer's directions (Cetus-Perkin-  
5 Elmer), except for the addition of 1 microgram of RNase A. The reactions were carried out in a final volume of 100 microliters. The PCR was performed for 35 cycles, utilizing a regimen of 37°C, 72°C, and 94°C.

The primers for cDNA synthesis and for the PCR  
10 reactions were derived from the HCV cDNA sequences in either clone 81, clone 36, or clone 37b. (The HCV cDNA sequences of clones 81, 36, and 37b are shown in Figs. 4, 5, and 10, respectively.) The sequences of the two 16-mer primers derived from clone 81 were:

15

5' CAA TCA TAC CTG ACA G 3'

and

5' GAT AAC CTC TGC CTG A 3'.

20 The sequence of the primer from clone 36 was:

5' GCA TGT CAT GAT GTA T 3'.

The sequence of the primer from clone 37b was:

25

5' ACA ATA CGT GTG TCA C 3'.

In the PCR reactions, the primer pairs consisted of either the two 16-mers derived from clone 81, or the 16-mer from  
30 clone 36 and the 16-mer from clone 37b.

The PCR reaction products were analyzed by separation of the products by alkaline gel electrophoresis, followed by Southern blotting, and detection of the amplified HCV-cDNA sequences with a <sup>32</sup>P-labeled internal oligonucleotide probe derived from a  
35

region of the HCV cDNA which does not overlap the primers. The PCR reaction mixtures were extracted with phenol/chloroform, and the nucleic acids precipitated from the aqueous phase with salt and ethanol. The precipitated 5 nucleic acids were collected by centrifugation, and dissolved in distilled water. Aliquots of the samples were subjected to electrophoresis on 1.8% alkaline agarose gels. Single stranded DNA of 60, 108, and 161 nucleotide lengths were co-electrophoresed on the gels as molecular 10 weight markers. After electrophoresis, the DNAs in the gel were transferred onto Biorad Zeta Probe™ paper. Prehybridization and hybridization, and wash conditions were those specified by the manufacturer (Biorad).

The probes used for the hybridization-detection 15 of amplified HCV cDNA sequences were the following. When the pair of PCR primers were derived from clone 81, the probe was an 108-mer with a sequence corresponding to that which is located in the region between the sequences of the two primers. When the pair of PCR primers were 20 derived from clones 36 and 37b, the probe was the nick-translated HCV cDNA insert derived from clone 35. The primers are derived from nucleotides 155-170 of the clone 37b insert, and 206-268 of the clone 36 insert. The 3'-end of the HCV cDNA insert in clone 35 overlaps 25 nucleotides 1-186 of the insert in clone 36; and the 5'-end of clone 35 insert overlaps nucleotides 207-269 of the insert in clone 37b. (Compare Figs. 5, 8 and 10.) Thus, the cDNA insert in clone 35 spans part of the region between the sequences of the clone 36 and 37b derived 30 primers, and is useful as a probe for the amplified sequences which include these primers.

Analysis of the RNA from the liver specimens was according to the above procedure utilizing both sets of primers and probes. The RNA from the liver of the three 35 chimpanzees with NANBH yielded positive hybridization

results for amplification sequences of the expected size (161 and 586 nucleotides for 81 and 36 and 37b, respectively), while the control chimpanzees yielded negative hybridization results. The same results were 5 achieved when the experiment was repeated three times.

Analysis of the nucleic acids and RNA from plasma was also according to the above procedure utilizing the primers and probe from clone 81. The plasmas were from two chimpanzees with NANBH, from a control 10 chimpanzee, and pooled plasmas from control chimpanzees. Both of the NANBH plasmas contained nucleic acids/RNA which yielded positive results in the PCR amplified assay, while both of the control plasmas yielded negative results. These results have been repeatably obtained 15 several times.

IV.D. Radioimmunoassay for Detecting HCV Antibodies in Serum from Infected Individuals

Solid phase radioimmunoassays to detect antibodies to HCV antigens were developed based upon Tsu and Herzenberg (1980). Microtiter plates (Immulon 2, Removawell strips) are coated with purified polypeptides containing HCV epitopes. The coated plates are incubated with either human serum samples suspected of containing 20 antibodies to the HCV epitopes, or to appropriate controls. During incubation, antibody, if present, is immunologically bound to the solid phase antigen. After removal of the unbound material and washing of the microtiter plates, complexes of human antibody-NANBV 25 antigen are detected by incubation with <sup>125</sup>I-labeled sheep anti-human immunoglobulin. Unbound labeled antibody is removed by aspiration, and the plates are washed. The radioactivity in individual wells is determined; the amount of bound human anti-HCV antibody is proportional to 30 the radioactivity in the well.

IV.D.1. Purification of Fusion Polypeptide SOD-NANB<sub>5-1-1</sub>.

The fusion polypeptide SOD-NANB<sub>5-1-1</sub>, expressed in recombinant bacteria as described in Section IV.B.1., was purified from the recombinant E. coli by differential extraction of the cell extracts with urea, followed by chromatography on anion and cation exchange columns as follows.

Thawed cells from 1 liter of culture were resuspended in 10 ml of 20% (w/v) sucrose containing 0.01M Tris HCl, pH 8.0, and 0.4 ml of 0.5M EDTA, pH 8.0 was added. After 5 minutes at 0°C, the mixture was centrifuged at 4,000 x g for 10 minutes. The resulting pellet was suspended in 10 ml of 25% (w/v) sucrose containing 0.05 M Tris HCl, pH 8.0, 1 mM phenylmethylsulfonylfluoride (PMSF) and 1 microgram/ml pepstatin A, followed by addition of 0.5 ml lysozyme (10 mg/ml) and incubation at 0°C for 10 minutes. After the addition of 10 ml 1% (v/v) Triton X-100 in 0.05 M Tris HCl, pH 8.0, 1 mM EDTA, the mixture was incubated an additional 10 min at 0°C with occasional shaking. The resulting viscous solution was homogenized by passage 6 times through a sterile 20-gauge hypodermic needle, and centrifuged at 13,000 x g for 25 minutes. The pelleted material was suspended in 5 ml of 0.01 M Tris HCl pH 8.0, and the suspension centrifuged at 4,000 x g for 10 minutes. The pellet, which contained SOD-NANB<sub>5-1-1</sub> fusion protein, was dissolved in 5 ml of 6 M urea in 0.02 M Tris HCl, pH 8.0, 1 mM dithiothreitol (Buffer A), and was applied to a column of Q-Sepharose Fast Flow equilibrated with Buffer A. Polypeptides were eluted with a linear gradient of 0.0 to 0.3 M NaCl in Buffer A. After elution, fractions were analyzed by polyacrylamide gel electrophoresis in the presence of SDS to determine their content of SOD-NANB<sub>5-1-1</sub>. Fractions containing this polypeptide were pooled, and dialyzed against 6 M urea in

-111-

0.02 M sodium phosphate buffer, pH 6.0, 1 mM dithiothreitol (Buffer B). The dialyzed sample was applied on a column of S-Sepharose Fast Flow equilibrated with Buffer B, and polypeptides eluted with a linear 5 gradient of 0.0 to 0.3 M NaCl in Buffer B. The fractions were analyzed by polyacrylamide gel electrophoresis for the presence of SOD-NANB<sub>5-1-1</sub>, and the appropriate fractions were pooled.

10 The final preparation of SOD-NANB<sub>5-1-1</sub> polypeptide was examined by electrophoresis on polyacrylamide gels in the presence of SDS. Based upon this analysis, the preparation was more than 80% pure.

15 IV.D.2. Purification of Fusion Polypeptide SOD-NANB<sub>81</sub>.  
The fusion polypeptide SOD-NANB<sub>81</sub>, expressed in recombinant bacteria as described in Section IV.B.2., was purified from recombinant E. coli by differential extraction of the cell extracts with urea, followed by chromatography on anion and cation exchange columns 20 utilizing the procedure described for the isolation of fusion polypeptide SOD-NANB<sub>5-1-1</sub> (See Section IV.D.1.).

25 The final preparation of SOD-NANB<sub>81</sub> polypeptide was examined by electrophoresis on polyacrylamide gels in the presence of SDS. Based upon this analysis, the preparation was more than 50% pure.

IV.D.3. Detection of Antibodies to HCV Epitopes by Solid Phase Radioimmunoassay.

Serum samples from 32 patients who were 30 diagnosed as having NANBH were analyzed by radioimmunoassay (RIA) to determine whether antibodies to HCV epitopes present in fusion polypeptides SOD-NANB<sub>5-1-1</sub> and SOD-NANB<sub>81</sub> were detected.

35 Microtiter plates were coated with SOD-NANB<sub>5-1-1</sub> or SOD-NANB<sub>81</sub>, which had been partially purified according

-112-

to Sections IV.D.1. and IV.D.2., respectively. The assays were conducted as follows.

One hundred microliter aliquots containing 0.1 to 0.5 micrograms of SOD-NANB<sub>5-1-1</sub> or SOD-NANB<sub>81</sub> in 0.125 M Na borate buffer, pH 8.3, 0.075 M NaCl (BBS) was added to each well of a microtiter plate (Dynatech Immulon 2 Removewell Strips). The plate was incubated at 4°C overnight in a humid chamber, after which, the protein solution was removed and the wells washed 3 times with BBS containing 0.02% Triton X-100 (BBST). To prevent non-specific binding, the wells were coated with bovine serum albumin (BSA) by addition of 100 microliters of a 5 mg/ml solution of BSA in BBS followed by incubation at room temperature for 1 hour; after this incubation the BSA solution was removed. The polypeptides in the coated wells were reacted with serum by adding 100 microliters of serum samples diluted 1:100 in 0.01M Na phosphate buffer, pH 7.2, 0.15 M NaCl (PBS) containing 10 mg/ml BSA, and incubating the serum containing wells for 1 hr at 37°C. After incubation, the serum samples were removed by aspiration, and the wells were washed 5 times with BBST. Anti-NANB<sub>5-1-1</sub> and Anti-NANB<sub>81</sub> bound to the fusion polypeptides was determined by the binding of <sup>125</sup>I-labeled F'(ab)<sub>2</sub> sheep anti-human IgG to the coated wells. Aliquots of 100 microliters of the labeled probe (specific activity 5-20 microcuries/microgram) were added to each well, and the plates were incubated at 37°C for 1 hour, followed by removal of excess probe by aspiration, and 5 washes with BBST. The amount of radioactivity bound in each well was determined by counting in a counter which detects gamma radiation.

The results of the detection of anti-NANB<sub>5-1-1</sub> and anti-NANB<sub>81</sub> in individuals with NANBH is presented in Table 1.

-113-

**Table 1**  
**Detection of Anti-S-1-1 and Anti-81 in Sera of**  
**NANB, HAV and HBV Hepatitis Patients**

	<u>Patient Reference Number</u>	<u>Diagnosis</u>	<u>S/N</u>	
			<u>Anti-S-1-1</u>	<u>Anti-81</u>
5	1. 28 <sup>1</sup>	Chronic NANB, IVD <sup>2</sup>	0.77	4.20
		Chronic NANB, IVD	1.14	5.14
		Chronic NANB, IVD	2.11	4.05
10	2. 29 <sup>1</sup>	AVH <sup>3</sup> , NANB, Sporadic	1.09	1.05
		Chronic, NANB	33.89	11.39
		Chronic, NANB	36.22	13.67
15	3. 30 <sup>1</sup>	AVH, NANB, IVD	1.90	1.54
		Chronic NANB, IVD	34.17	30.28
		Chronic NANB, IVD	32.45	30.84
20	4. 31	Chronic NANB, PT <sup>4</sup>	16.09	8.05
		Late AVH NANB, IVD	0.69	0.94
		Late AVH NANB, IVD	0.73	0.68
25	5. 32 <sup>1</sup>	AVH, NANB, IVD	1.66	1.96
		AVH, NANB, IVD	1.53	0.56
		Chronic NANB, PT	34.40	7.55
30	6. 33 <sup>1</sup>	Chronic NANB, PT	45.55	13.11
		Chronic NANB, PT	41.58	13.45
		Chronic NANB, PT	44.20	15.48
35	7. 34 <sup>1</sup>	AVH NANB, IVD	31.92	31.95
		"Healed" recent NANB, AVH	6.87	4.45
		Late AVH NANB PT	11.84	5.79
40	8. 35 <sup>1</sup>	AVH NANB, IVD	6.52	1.33
		Late AVH NANB, PT	39.44	39.18
		Chronic NANB, PT	42.22	37.54
45	9. 36	AVH, NANB, PT	1.35	1.17
		Chronic NANB? PT	0.35	0.28

-114-

<u>Patient Reference Number</u>	<u>Diagnosis</u>	<u>S/N</u>	
		<u>Anti-5-1-1</u>	<u>Anti-81</u>
15. 42	AVH, NANB, IVD	6.25	2.34
5 16. 43	Chronic NANB, PT	0.74	0.61
17. 44	AVH, NANB, PT	5.40	1.83
18. 45	Chronic, NANB, PT	0.52	0.32
19. 46	AVH, NANB	23.35	4.45
10 20. 47	AVH, Type A	1.60	1.35
21. 48	AVH, Type A	1.30	0.66
22. 49	AVH, Type A	1.44	0.74
23. 50	Resolved Recent AVH, Type A	0.48	0.56
15 24. 51	AVH, Type A Resolved AVH, Type A	0.68 0.80	0.64 0.65
25. 52	Resolved Recent AVH, Type A Resolved Recent AVH, Type A	1.38 0.80	1.04 0.65
20 26. 53	AVH, Type A Resolved Recent AVH, Type A	1.85 1.02	1.16 0.88
27. 54	AVH, Type A	1.35	0.74
28. 55	Late AVH, HBV	0.58	0.55
25 29. 56	Chronic HBV	0.84	1.06
30. 57	Late AVH, HBV	3.20	1.60
31. 58	Chronic HBV	0.47	0.46
32. 59 <sup>1</sup>	AVH, HBV Healed AVH, HBV	0.73 0.43	0.60 0.44
30 33. 60 <sup>1</sup>	AVH, HBV Healed AVH, HBV	1.06 0.75	0.92 0.68

-115-

	Patient Reference Number	Diagnosis	S/N	
			Anti-5-1-1	Anti-81
5	34. 61 <sup>1</sup>	AVH, HBV Healed AVH, HBV	1.66 0.63	0.61 0.36
	35. 62 <sup>1</sup>	AVH, HBV Healed AVH, HBV	1.02 0.41	0.73 0.42
10	36. 63 <sup>1</sup>	AVH, HBV Healed AVH, HBV	1.24 1.55	1.31 0.45
	37. 64 <sup>1</sup>	AVH, HBV Healed AVH, HBV	0.82 0.53	0.79 0.37
	38. 65 <sup>1</sup>	AVH, HBV Healed AVH, HBV	0.95 0.70	0.92 0.50
15	39. 66 <sup>1</sup>	AVH, HBV Healed AVH, HBV	1.03 1.71	0.68 1.39

<sup>1</sup> Sequential serum samples available from these patients

<sup>2</sup> IVD=Intravenous Drug User

<sup>3</sup> AVH=Acute viral hepatitis

<sup>4</sup> PT=Post transfusion

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-116-

As seen in Table 1, 19 of 32 sera from patients diagnosed as having NANBH were positive with respect to antibodies directed against HCV epitopes present in SOD-NANB<sub>5-1-1</sub> and SOD-NANB<sub>81</sub>.

5 However, the serum samples which were positive were not equally immunologically reactive with SOD-NANB<sub>5-1-1</sub> and SOD-NANB<sub>81</sub>. Serum samples from patient No. 1 were positive to SOD-NANB<sub>81</sub> but not to SOD-NANB<sub>5-1-1</sub>. Serum samples from patients number 10, 15, and 17 were positive  
10 to SOD-NANB<sub>5-1-1</sub> but not to SOD-NANB<sub>81</sub>. Serum samples from patients No. 3, 8, 11, and 12 reacted equally with both fusion polypeptides, whereas serum samples from patients No. 2, 4, 7, and 9 were 2-3 fold higher in the reaction to SOD-NANB<sub>5-1-1</sub> than to SOD-NANB<sub>81</sub>. These  
15 results suggest that NANB<sub>5-1-1</sub> and NANB<sub>81</sub> may contain at least 3 different epitopes; i.e., it is possible that each polypeptide contains at least 1 unique epitope, and that the two polypeptides share at least 1 epitope.

20 IV.D.4. Specificity of the Solid Phase RIA for NANBH

The specificity of the solid phase RIAs for NANBH was tested by using the assay on serum from patients infected with HAV or with HBV and on sera from control individuals. The assays utilizing partially purified SOD-  
25 NANB<sub>5-1-1</sub> and SOD-NANB<sub>81</sub> were conducted essentially as described in Section IV.D.3, except that the sera was from patients previously diagnosed as having HAV or HBV, or from individuals who were blood bank donors. The results for sera from HAV and HBV infected patients are presented  
30 in table 1. The RIA was tested using 11 serum specimens from HAV infected patients, and 20 serum specimens from HBV infected patients. As shown in table 1, none of these sera yielded a positive immunological reaction with the fusion polypeptides containing BB-NANBV epitopes.

-117-

The RIA using the NANB<sub>5-1-1</sub> antigen was used to determine immunological reactivity of serum from control individuals. Out of 230 serum samples obtained from the normal blood donor population, only 2 yielded positive reactions in the RIA (data not shown). It is possible that the two blood donors from whom these serum samples originated had previously been exposed to HCV.

10 IV.D.5. Reactivity of NANB<sub>5-1-1</sub> During the Course of NANBH Infection.

15 The presence of anti-NANB<sub>5-1-1</sub> antibodies during the course of NANBH infection of 2 patients and 4 chimpanzees was followed using RIA as described in Section IV.D.3. In addition the RIA was used to determine the presence or absence of anti-NANB<sub>5-1-1</sub> antibodies during the course of infection of HAV and HBV in infected chimpanzees.

20 The results, which are presented in Table 2, show that with chimpanzees and with humans, anti-NANB<sub>5-1-1</sub> antibodies were detected following the onset of the acute phase of NANBH infection. Anti-NANB<sub>5-1-1</sub> antibodies were not detected in serum samples from chimpanzees infected with either HAV or HBV. Thus anti-NANB<sub>5-1-1</sub> antibodies serve as a marker for an individual's exposure to HCV.

-118-

**Table 2**  
**Seroconversion in Sequential Serum Samples from**  
**Hepatitis Patients and Chimpanzees Using S-I-I Antigen**

Patient/ Chimp	Sample Date (Days) (0=inoculation day)	Hepatitis Viruses	Anti-S-I-I (S/N)	ALT (mu/ml)
5 Patient 29	T <sup>0</sup>	NANB	1.09	1180
	T+180		33.89	425
	T+208		36.22	--
10 Patient 30	T	NANB	1.90	1830
	T+307		34.17	290
	T+799		32.45	276
10 Chimp 1	0	NANB	0.87	9
	76		0.93	71
	118		23.67	19
	154		32.41	--
10 Chimp 2	0	NANB	1.00	5
	21		1.08	52
	73		4.64	13
	138		25.01	--
15 Chimp 3	0	NANB	1.08	8
	43		1.44	205
	53		1.82	14
	159		11.87	6
20 Chimp 4	-3	NANB	1.12	11
	55		1.25	132
	83		6.60	--
	140		17.51	--
20 Chimp 5	0	HAV	1.50	4
	25		2.39	147
	40		1.92	18
	268		1.53	5
25 Chimp 6	-8	HAV	0.85	--
	15		--	106
	41		0.81	10
	129		1.33	--

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-119-

	Patient/ Chimp	Sample Date (Days) (0 = inoculation day)	Hepatitis Viruses	Anti-S-I-I (S/N)	ALT (mu/ml)
5	Chimp 7	0	HAV	1.17	7
		22		1.60	83
		115		1.55	5
		139		1.60	--
10	Chimp 8	0	HAV	0.77	15
		26		1.98	130
		74		1.77	8
		205		1.27	5
15	Chimp 9	-290	HBV	1.74	--
		379		3.29	9
		435		2.77	6
		0		2.35	8
20	Chimp 10	111-118 (pool)	HBV	2.74	95-155 (pool)
		205		2.05	9
		240		1.78	13
		0		1.82	11
25	Chimp 11	28-56 (pool)	HBV	1.26	8-100 (pool)
		169		--	9
		223		0.52	10

20 \*T=day of initial sampling

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-120-

IV.E. Purification of Polyclonal Serum Antibodies to NANB<sub>5-1-1</sub>

On the basis of the specific immunological reactivity of the SOD-NANB<sub>5-1-1</sub> polypeptide with the antibodies in serum samples from patients with NANBH, a method was developed to purify serum antibodies which react immunologically with the epitope(s) in NANB<sub>5-1-1</sub>. This method utilizes affinity chromatography. Purified SOD-NANB<sub>5-1-1</sub> polypeptide (see Section IV.D.1) was attached to an insoluble support; the attachment is such that the immobilized polypeptide retains its affinity for antibody to NANB<sub>5-1-1</sub>. Antibody in serum samples is absorbed to the matrix-bound polypeptide. After washing to remove non-specifically bound materials and unbound materials, the bound antibody is released from the bound SOD-HCV polypeptide by change in pH, and/or by chaotropic reagents, for example, urea.

Nitrocellulose membranes containing bound SOD-NANB<sub>5-1-1</sub> were prepared as follows. A nitrocellulose membrane, 2.1 cm Sartorius of 0.2 micron pore size, was washed for 3 minutes three times with BBS. SOD-NANB<sub>5-1-1</sub> was bound to the membrane by incubation of the purified preparation in BBS at room temperature for 2 hours; alternatively it was incubated at 4°C overnight. The solution containing unbound antigen was removed, and the filter was washed three times with BBS for three minutes per wash. The remaining active sites on the membrane were blocked with BSA by incubation with a 5 mg/ml BSA solution for 30 minutes. Excess BSA was removed by washing the membrane with 5 times with BBS and 3 times with distilled water. The membrane containing the viral antigen and BSA was then treated with 0.05 M glycine hydrochloride, pH 2.5, 0.10 M NaCl (GlyHCl) for 15 minutes, followed by 3 three minute washes with PBS.

-121-

5 Polyclonal anti-NANB<sub>5-1-1</sub> antibodies were isolated by incubating the membranes containing the fusion polypeptide with serum from an individual with NANBH for 2 hours. After the incubation, the filters were washed 5 times with BBS, and twice with distilled water. Bound antibodies were then eluted from each filter with 5 elutions of GlyHCl, at 3 minutes per elution. The pH of the eluates was adjusted to pH 8.0 by collecting each eluate in a test tube containing 2.0 M Tris HCl, pH 8.0.

10 Recovery of the anti-NANB<sub>5-1-1</sub> antibody after affinity chromatography is approximately 50%.

15 The nitrocellulose membranes containing the bound viral antigen can be used several times without appreciable decrease in binding capacity. To reuse the membranes, after the antibodies have been eluted the membranes are washed with BBS three times for 3 minutes. They are then stored in BBS at 4°C.

IV.F. The Capture of HCV Particles from Infected Plasma  
20 Using Purified Human Polyclonal Anti-HCV Antibodies;  
Hybridization of the Nucleic Acid in the Captured  
Particles to HCV cDNA

IV.F.1. The Capture of HCV Particles from Infected Plasma  
25 Using Human Polyclonal Anti-HCV Antibodies

Protein-nucleic acid complexes present in infectious plasma of a chimpanzee with NANBH were isolated using purified human polyclonal anti-HCV antibodies which were bound to polystyrene beads.

30 Polyclonal anti-NANB<sub>5-1-1</sub> antibodies were purified from serum from a human with NANBH using the SOD-HCV polypeptide encoded in clone 5-1-1. The method for purification was that described in Section IV.E.

35 The purified anti-NANB<sub>5-1-1</sub> antibodies were bound to polystyrene beads (1/4" diameter, specular fin-

-122-

ish, Precision Plastic Ball Co., Chicago, Illinois) by incubating each at room temperature overnight with 1 ml of antibodies (1 microgram/ml in borate buffered saline, pH 8.5). Following the overnight incubation, the beads were 5 washed once with TBST [50 mM Tris HCl, pH 8.0, 150 mM NaCl, 0.05% (v/v) Tween 20], and then with phosphate buffered saline (PBS) containing 10 mg/ml BSA.

Control beads were prepared in an identical fashion, except that the purified anti-NANB<sub>5-1-1</sub> antibodies 10 were replaced with total human immunoglobulin.

Capture of HCV from NANBH infected chimpanzee plasma using the anti-NANB<sub>5-1-1</sub> antibodies bound to beads was accomplished as follows. The plasma from a chimpanzee with NANBH used is described in Section IV.A.1.. An 15 aliquot (1 ml) of the NANBV infected chimpanzee plasma was incubated for 3 hours at 37°C with each of 5 beads coated with either anti-NANB<sub>5-1-1</sub> antibodies, or with control immunoglobulins. The beads were washed 3 times with TBST.

20 IV.F.2. Hybridization of the Nucleic Acid in the Captured Particles to NANBV-cDNA

The nucleic acid component released from the particles captured with anti-NANB<sub>5-1-1</sub> antibodies was analyzed for hybridization to HCV cDNA derived from clone 25 81.

HCV particles were captured from NANBH infected chimpanzee plasma, as described in IV.F.1. To release the nucleic acids from the particles, the washed beads were incubated for 60 min. at 37°C with 0.2 ml per bead of a 30 solution containing proteinase k (1 mg/ml), 10 mM Tris HCl, pH 7.5, 10 mM EDTA, 0.25% (w/v) SDS, 10 micrograms/ml soluble yeast RNA, and the supernatant solution was removed. The supernatant was extracted with phenol and chloroform, and the nucleic acids precipitated with 35 ethanol overnight at -20°C. The nucleic acid precipitate

-123-

was collected by centrifugation, dried, and dissolved in 50 mM Hepes, pH 7.5. Duplicate aliquots of the soluble nucleic acids from the samples obtained from beads coated with anti-NANB<sub>5-1-1</sub> antibodies and with control beads containing total human immunoglobulin were filtered onto to nitrocellulose filters. The filters were hybridized with a <sup>32</sup>P-labeled, nick-translated probe made from the purified HCV cDNA fragment in clone 81. The methods for preparing the probe and for the hybridization are described in Section IV.C.1..

Autoradiographs of a probed filter containing the nucleic acids from particles captured by beads containing anti-NANB<sub>5-1-1</sub> antibodies are shown in Fig. 40. The extract obtained using the anti-NANB<sub>5-1-1</sub> antibody (A<sub>1</sub>, A<sub>2</sub>) gave clear hybridization signals relative to the control antibody extract (A<sub>3</sub>, A<sub>4</sub>) and to control yeast RNA (B<sub>1</sub>, B<sub>2</sub>). Standards consisting of 1pg, 5pg, and 10pg of the purified, clone 81 cDNA fragment are shown in C1-3, respectively.

These results demonstrate that the particles captured from NANBH plasma by anti-NANB<sub>5-1-1</sub>-antibodies contain nucleic acids which hybridize with HCV cDNA in clone 81, and thus provide further evidence that the cDNAs in these clones are derived from the etiologic agent for NANBH.

IV.G. Immunological Reactivity of C100-3 with Purified Anti-NANB<sub>5-1-1</sub> Antibodies

The immunological reactivity of C100-3 fusion polypeptide with anti-NANB<sub>5-1-1</sub> antibodies was determined by a radioimmunoassay, in which the antigens which were bound to a solid phase were challenged with purified anti-NANB<sub>5-1-1</sub> antibodies, and the antigen-antibody complex detected with <sup>125</sup>I-labeled sheep anti-human antibodies.

-124-

The immunological reactivity of C100-3 polypeptide was compared with that of SOD-NANB<sub>5-1-1</sub> antigen.

5 The fusion polypeptide C100-3 was synthesized and purified as described in Section IV.B.5. and in Section IV.B.6., respectively. The fusion polypeptide SOD-NANB<sub>5-1-1</sub> was synthesized and purified as described in Section IV.B.1. and in Section IV.D.1., respectively.

Purified anti-NANB<sub>5-1-1</sub> antibodies were obtained as described in Section IV.E.

10 One hundred microliter aliquots containing varying amounts of purified C100-3 antigen in 0.125M Na borate buffer, pH 8.3, 0.075M NaCl (BBS) was added to each well of a microtiter plate (Dynatech Immulon 2 Removawell Strips). The plate was incubated at 4°C overnight in a  
15 humid chamber, after which, the protein solution was removed and the wells washed 3 times with BBS containing 0.02% Triton X-100 (BBST). To prevent non-specific binding, the wells were coated with BSA by addition of 100 microliters of a 5 mg/ml solution of BSA in BBS followed  
20 by incubation at room temperature for 1 hour, after which the excess BSA solution was removed. The polypeptides in the coated wells were reacted with purified anti-NANB<sub>5-1-1</sub> antibodies by adding 1 microgram antibody/well, and incubating the samples for 1 hr at 37°C. After incubation,  
25 the excess solution was removed by aspiration, and the wells were washed 5 times with BBST. Anti-NANB<sub>5-1-1</sub> bound to the fusion polypeptides was determined by the binding of <sup>125</sup>I-labeled F'(ab)<sub>2</sub> sheep anti-human IgG to the coated wells. Aliquots of 100 microliters of the  
30 labeled probe (specific activity 5-20 microcuries/microgram) were added to each well, and the plates were incubated at 37°C for 1 hour, followed by removal of excess probe by aspiration, and 5 washes with BBST. The amount of radioactivity bound in each well was determined  
35 by counting in a counter which detects gamma radiation.

-125-

The results of the immunological reactivity of C100 with purified anti-NANB<sub>5-1-1</sub> as compared to that of NANB<sub>5-1-1</sub> with the purified antibodies are shown in Table 3.

5

Table 3  
Immunological Reactivity of C100-3 compared to NANB<sub>5-1-1</sub>  
by Radioimmunoassay

10

AG(ng)	RIA (cpm/assay)						0
	400	320	240	160	60		
NANB <sub>5-1-1</sub>	7332	6732	4954	4050	3051	57	
C100-3	7450	6985	5920	5593	4096	67	

15

The results in Table 3 show that anti-NANB<sub>5-1-1</sub> recognizes an epitope(s) in the C100 moiety of the C100-3 polypeptide. Thus NANB<sub>5-1-1</sub> and C100 share a common 20 epitope(s). The results suggest that the cDNA sequence encoding this NANBV epitope(s) is one which is present in both clone 5-1-1 and in clone 81.

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#### IV.H. Characterization of HCV

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##### IV.H.1. Characterization of the Strandedness of the HCV Genome.

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The HCV genome was characterized with respect to its strandedness by isolating the nucleic acid fraction from particles captured on anti-NANB<sub>5-1-1</sub> antibody coated polystyrene beads, and determining whether the isolated nucleic acid hybridized with plus and/or minus strands of HCV cDNA.

35

Particles were captured from HCV infected chimpanzee plasma using polystyrene beads coated with

-126-

immunopurified anti-NANB<sub>5-1-1</sub> antibody as described in Section IV.F.1. The nucleic acid component of the particles was released using the method described in Section IV.F.2. Aliquots of the isolated genomic nucleic acid equivalent to 3 mls of high titer plasma were blotted onto nitrocellulose filters. As controls, aliquots of denatured HCV cDNA from clone 81 (2 picograms) was also blotted onto the same filters. The filters were probed with <sup>32</sup>P-labeled mixture of plus or mixture of minus 10 strands of single stranded DNA cloned from HCV cDNAs; the cDNAs were excised from clones 40b, 81, and 25c.

The single stranded probes were obtained by excising the HCV cDNAs from clones 81, 40b, and 25c with EcoRI, and cloning the cDNA fragments in M13 vectors, mp18 15 and mp19 [Messing (1983)]. The M13 clones were sequenced to determine whether they contained the plus or minus strands of DNA derived from the HCV cDNAs. Sequencing was by the dideoxychain termination method of Sanger et al. (1977).

Each of a set of duplicate filters containing aliquots of the HCV genome isolated from the captured particles was hybridized with either plus or minus strand probes derived from the HCV cDNAs. Fig. 41 shows the autoradiographs obtained from probing the NANBV genome 25 with the mixture of probes derived from clones 81, 40b, and 25c. This mixture was used to increase the sensitivity of the hybridization assay. The samples in panel I were hybridized with the plus strand probe mixture. The samples in panel II were probed by hybridization with the 30 minus strand probe mixture. The composition of the samples in the panels of the immunoblot are presented in table 4.

-127-

Table 4

	lane	A	B
5	1	HCV genome	*
	2	----	*
10	3	*	cDNA 81
	4	----	cDNA 81

15 \* is an undescribed sample.

As seen from the results in Fig. 41, only the minus strand DNA probe hybridizes with the isolated HCV genome. This result, in combination with the result showing that the genome is sensitive to RNase and not DNase (See Section IV.C.2.), suggests that the genome of NANBV is positive stranded RNA.

These data, and data from other laboratories concerning the physicochemical properties of a putative NANBV(s), are consistent with the possibility that HCV is a member of the Flaviviridae. However, the possibility that HCV represents a new class of viral agent has not been eliminated.

30 IV.H.2. Detection of Sequences in Captured Particles Which When Amplified by PCR Hybridize to HCV cDNA Derived from Clone 81

The RNA in captured particles was obtained as described in Section IV.H.1. The analysis for sequences which hybridize to the HCV cDNA derived from clone 81 was

-128-

carried out utilizing the PCR amplification procedure, as described in Section IV.C.3, except that the hybridization probe was a kinased oligonucleotide derived from the clone 81 cDNA sequence. The results showed that the amplified 5 sequences hybridized with the clone 81 derived HCV cDNA probe.

IV.H.3. Homology Between the Non-Structural Protein of Dengue Flavivirus (MNWWVD1) and the HCV Polypeptides Encoded by the Combined ORF of Clones 14i Through 39c

The combined HCV cDNAs of clones 14i through 39c contain one continuous ORF, as shown in Fig. 26. The polypeptide encoded therein was analyzed for sequence homology with the region of the non-structural 15 polypeptide(s) in Dengue flavivirus (MNWVD1). The analysis used the Dayhoff protein data base, and was performed on a computer. The results are shown in Fig. 42, where the symbol (:) indicates an exact homology, and the symbol (.) indicates a conservative replacement in the 20 sequence; the dashes indicate spaces inserted into the sequence to achieve the greatest homologies. As seen from the figure, there is significant homology between the sequence encoded in the HCV cDNA, and the non-structural polypeptide(s) of Dengue virus. In addition to the homology shown in Fig. 42, analysis of the polypeptide segment 25 encoded in a region towards the 3'-end of the cDNA also contained sequences which are homologous to sequences in the Dengue polymerase. Of consequence is the finding that the canonical Gly-Asp-Asp (GDD) sequence thought to be 30 essential for RNA-dependent RNA polymerases is contained in the polypeptide encoded in HCV cDNA, in a location which is consistent with that in Dengue 2 virus. (Data not shown.)

IV.H.4. HCV-DNA is Not Detectable in NANBH Infected Tissue

Two types of studies provide results suggesting that HCV-DNA is not detectable in tissue from an individual with NANBH. These results, in conjunction with 5 those described in IV.C. and IV.H.1. and IV.H.2. provide evidence that HCV is not a DNA containing virus, and that its replication does not involve cDNA.

IV.H.4.a. Southern Blotting Procedure

10 In order to determine whether NANBH infected chimpanzee liver contains detectable HCV-DNA (or HCV-cDNA), restriction enzyme fragments of DNA isolated from this source was Southern blotted, and the blots probed with <sup>32</sup>P-labeled HCV cDNA. The results showed that the 15 labeled HCV cDNA did not hybridize to the blotted DNA from the infected chimpanzee liver. It also did not hybridize to control blotted DNA from normal chimpanzee liver. In contrast, in a positive control, a labeled probe of the beta-interferon gene hybridized strongly to Southern blots 20 of restriction enzyme digested human placental DNA. These systems were designed to detect a single copy of the gene which was to be detected with the labeled probe.

DNAs were isolated from the livers of two chimpanzees with NANBH. Control DNAs were isolated from 25 uninfected chimpanzee liver, and from human placentas. The procedure for extracting DNA was essentially according to Maniatis et al. (1982), and the DNA samples were treated with RNase during the isolation procedure.

Each DNA sample was treated with either EcoRI, 30 MboI, or HincII (12 micrograms), according to the manufacturer's directions. The digested DNAs were electrophoresed on 1% neutral agarose gels, Southern blotted onto nitrocellulose, and the blotted material 35 hybridized with the appropriate nick-translated probe cDNA ( $3 \times 10^6$  cpm/ml of hybridization mix). The DNA from

-130-

infected chimpanzee liver and normal liver were hybridized with  $^{32}\text{P}$ -labeled HCV cDNA from clones 36 plus 81; the DNA from human placenta was hybridized with  $^{32}\text{P}$ -labeled DNA from the beta-interferon gene. After hybridization, the 5 blots were washed under stringent conditions, i.e., with a solution containing 0.1 x SSC, 0.1% SDS, at 65°C.

The beta-interferon gene DNA was prepared as described by Houghton et al (1981).

10 IV.H.4.b. Amplification by the PCR Technique

In order to determine whether HCV-DNA could be detected in liver from chimpanzees with NANBH, DNA was isolated from the tissue, and subjected to the PCR amplification-detection technique using primers and probe 15 polynucleotides derived from HCV cDNA from clone 81.

Negative controls were DNA samples isolated from uninfected HepG2 tissue culture cells, and from presumably uninfected human placenta. Positive controls were samples 20 of the negative control DNAs to which a known relatively small amount (250 molecules) of the HCV cDNA insert from clone 81 was added.

In addition, to confirm that RNA fractions isolated from the same livers of chimpanzees with NANBH contained sequences complementary to the HCV-cDNA probe, 25 the PCR amplification-detection system was also used on the isolated RNA samples.

In the studies, the DNAs were isolated by the procedure described in Section IV.H.4.a, and RNAs were extracted essentially as described by Chirgwin et al. 30 (1981).

Samples of DNA were isolated from 2 infected chimpanzee livers, from uninfected HepG2 cells, and from human placenta. One microgram of each DNA was digested with HindIII according to the manufacturer's directions. 35 The digested samples were subjected to PCR amplification

and detection for amplified HCV cDNA essentially as described in Section IV.C.3., except that the reverse transcriptase step was omitted. The PCR primers and probe were from HCV cDNA clone 81, and are described in Section 5 IV.C.3.. Prior to the amplification, for positive controls, a one microgram sample of each DNA was "spiked" by the addition of 250 molecules of HCV cDNA insert isolated from clone 81.

In order to determine whether HCV sequences were 10 present in RNA isolated from the livers of chimpanzees with NANBH, samples containing 0.4 micrograms of total RNA were subjected to the amplification procedure essentially as described in Section IV.C.3., except that the reverse transcriptase was omitted from some of the samples as a 15 negative control. The PCR primers and probe were from HCV cDNA clone 81, as described supra.

The results showed that amplified sequences complementary to the HCV cDNA probe were not detectable in the DNAs from infected chimpanzee liver, nor were they 20 detectable in the negative controls. In contrast, when the samples, including the DNA from infected chimpanzee liver, was spiked with the HCV cDNA prior to amplification, the clone 81 sequences were detected in all 25 positive control samples. In addition, in the RNA studies, amplified HCV cDNA clone 81 sequences were detected only when reverse transcriptase was used, suggesting strongly that the results were not due to a DNA contamination.

These results show that hepatocytes from 30 chimpanzees with NANBH contain no, or undetectable levels, of HCV DNA. Based upon the spiking study, if HCV DNA is present, it is at a level far below .06 copies per hepatocyte. In contrast, the HCV sequences in total RNA from the same liver samples was readily detected with the 35 PCR technique.

-132-

IV.I. ELISA Determinations for HCV Infection Using HCV c100-3 As Test Antigen

All samples were assayed using the HCV c100-3 ELISA. This assay utilizes the HCV c100-3 antigen (which was synthesized and purified as described in Section 5 IV.B.5), and a horseradish peroxidase (HRP) conjugate of mouse monoclonal anti-human IgG.

Plates coated with the HCV c100-3 antigen were prepared as follows. A solution containing Coating buffer 10 (50mM Na Borate, pH 9.0), 21 ml/plate, BSA (25 micrograms/ml), c100-3 (2.50 micrograms/ml) was prepared just prior to addition to the Removeawell Immulon I plates (Dynatech Corp.). After mixing for 5 minutes, 0.2ml/well of the solution was added to the plates, they were covered and 15 incubated for 2 hours at 37°C, after which the solution was removed by aspiration. The wells were washed once with 400 microliters Wash Buffer (100 mM sodium phosphate, pH 7.4, 140 mM sodium chloride, 0.1% (W/V) casein, 1% (W/V) Triton x-100, 0.01% (W/V) Thimerosal). After removal 20 of the wash solution, 200 microliters/well of Postcoat solution (10 mM sodium phosphate, pH 7.2, 150 mM sodium chloride, 0.1% (w/v) casein and 2 mM phenylmethylsulfonylfluoride (PMSF)) was added, the plates were loosely covered to prevent evaporation, and were allowed to stand at room temperature for 30 minutes. The 25 wells were then aspirated to remove the solution, and lyophilized dry overnight, without shelf heating. The prepared plates may be stored at 2-8°C in sealed aluminum pouches.

In order to perform the ELISA determination, 20 microliters of serum sample or control sample was added to a well containing 200 microliters of sample diluent (100 mM sodium phosphate, pH 7.4, 500 mM sodium chloride, 1 mM EDTA, 0.1% (W/V) Casein, 0.015 (W/V) Therosal, 1% (W/V) Triton X-100, 100 micrograms/ml yeast extract). The 35

plates were sealed, and incubated at 37°C for two hours, after which the solution was removed by aspiration, and the wells were washed with 400 microliters of wash buffer (phosphate buffered saline (PBS) containing 0.05% Tween 5 20). The washed wells were treated with 200 microliters of mouse anti-human IgG-HRP conjugate contained in a solution of Ortho conjugate diluent (10 mM sodium phosphate, pH 7.2, 150 mM sodium chloride, 50% (V/V) fetal bovine serum, 1% (V/V) heat treated horse serum, 1 mM K<sub>3</sub>Fe(CN)<sub>6</sub>, 10 0.05% (W/V) Tween 20, 0.02% (W/V) Thimerosal). Treatment was for 1 hour at 37°C, the solution was removed by aspiration, and the wells were washed with wash buffer, which was also removed by aspiration. To determine the amount of bound enzyme conjugate, 200 microliters of 15 substrate solution (10 mg O-phenylenediamine dihydrochloride per 5 ml of Developer solution) was added. Developer solution contains 50 mM sodium citrate adjusted to pH 5.1 with phosphoric acid, and 0.6 microliters/ml of 30% H<sub>2</sub>O<sub>2</sub>. The plates containing the substrate solution 20 were incubated in the dark for 30 minutes at room temperature, the reactions were stopped by the addition of 50 microliters/ml 4N sulfuric acid, and the ODs determined.

The examples provided below show that the 25 microtiter plate screening ELISA which utilizes HCV c100-3 antigen has a high degree of specificity, as evidenced by an initial rate of reactivity of about 1%, with a repeat reactive rate of about 0.5% on random donors. The assay is capable of detecting an immunoresponse in both the post 30 acute phase of the infection, and during the chronic phase of the disease. In addition, the assay is capable of detecting some samples which score negative in the surrogate tests for NANBH; these samples come from individuals with a history of NANBH, or from donors 35 implicated in NANBH transmission.

In the examples described below, the following abbreviations are used:

	ALT	Alanine amino transferase
5	Anti-HBc	Antibody against HBc
	Anti-HBsAg	Antibody against HBsAg
	HBc	Hepatitis B core antigen
	ABsAg	Hepatitis B surface antigen
	IgG	Immunoglobulin G
10	IgM	Immunoglobulin M
	IU/L	International units/Liter
	NA	Not available
	NT	Not tested
	N	Sample size
15	Neg	Negative
	OD	Optical density
	Pos	Positive
	S/CO	Signal/cutoff
	SD	Standard deviation
20	x	Average or mean
	WNL	Within normal limits

IV.I.1. HCV Infection in a Population of Random Blood Donors

25 A group of 1,056 samples (fresh sera) from random blood donors were obtained from Irwin Memorial Blood Bank, San Francisco, California. The test results obtained with these samples are summarized in a histogram showing the distribution of the OD values (Fig. 43). As seen in Fig. 43, 4 samples read >3, 1 sample reads between 1 and 3, 5 samples read between 0.4 and 1, and the remaining 1,046 samples read <0.4, with over 90% of these samples reading <0.1.

35 The results on the reactive random samples are presented in Table 5. Using a cut-off value equal to the

-135-

mean plus 5 standard deviations, ten samples out of the 1,056 (0.95%) were initially reactive. Of these, five samples (0.47%) repeated as reactive when they were assayed a second time using the ELISA. Table 5 also shows 5 the ALT and Anti-HBd status for each of the repeatedly reactive samples. Of particular interest is the fact that all five repeat reactive samples were negative in both surrogate tests for NANBH, while scoring positive in the HCV ELISA.

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-136-

TABLE 5  
RESULTS ON REACTIVE RANDOM SAMPLES

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$N = 1051$   
 $\bar{x} = 0.049*$   
 $SD = \pm 0.074$   
 Cut-off:  $\bar{x} + 5SD = 0.419$  (0.400 + Negative Control)

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	<u>Samples</u>	Initial Reactives		Repeat Reactives		<u>Anti HBc*** (OD)</u>
		<u>OD</u>		<u>OD</u>		
	4227	0.462		0.084		NA
	6292	0.569		0.294		NA
15	6188	0.699		0.326		NA
	6157	0.735		0.187		NA
	6277	0.883		0.152		NA
	6397	1.567		1.392		30.14
	6019	>3.000		>3.000		46.48
	6651	>3.000		>3.000		48.53
	6669	>3.000		>3.000		60.53
20	4003	>3.000		3.000		WNL**** Negative
		10/1056 = 0.95%		5/1056 = 0.47%		

\* Samples reading >1.5 were not included in calculating the Mean and SD

\*\* ALT  $\geq$  68 IU/L is above normal limits.

25 \*\*\* Anti-HBc  $\leq$  0.535 (competition assay) is considered positive.

\*\*\*\* WNL: Within normal limits.

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#### IV.I.2. Chimpanzee Serum Samples

Serum samples from eleven chimpanzees were tested with the HCV c100-3 ELISA. Four of these 5 chimpanzees were infected with NANBH from a contaminated batch of Factor VIII (presumably Hutchinson strain), following an established procedure in a collaboration with Dr. Daniel Bradley at the Centers for Disease Control. As controls, four other chimpanzees were infected with HAV 10 and three with HBV. Serum samples were obtained at different times after infection.

The results, which are summarized in Table 6, show documented antibody seroconversion in all chimpanzees infected with the Hutchinson strain of NANBH. Following 15 the acute phase of infection (as evidenced by the significant rise and subsequent return to normal of ALT levels), antibodies to HCV c100-3 became detectable in the sera of the 4/4 NANBH infected chimpanzees. These samples had previously been shown, as discussed in Section 20 IV.B.3., to be positive by a Western analysis, and an RIA. In contrast, none of the control chimpanzees which had been infected with HAV or HBV showed evidence of reactivity in the ELISA.

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-138-

TABLE 6  
CHIMPANZEE SERUM SAMPLES

		<u>OD</u>	<u>S/CO</u>	<u>INOCULATION DATE</u>	<u>BLEED DATE</u>	<u>ALT (IU/L)</u>	<u>TRANSFUSED</u>
5	NEGATIVE CONTROL	0.001					
	POSITIVE CONTROL	1.501					
	CUTOFF	0.401					
	<u>Chimp 1</u>	-0.007 0.003 >3.000 >3.000	0.00 0.01 >7.48 >7.48	05/24/84	05/24/84 08/07/84 09/18/84 10/24/84	9 71 19 —	NANB
10							
	<u>Chimp 2</u>	---	---	06/07/84	—	—	NANB
		-0.003 -0.005 0.945 >3.000	0.00 0.00 2.36 >7.48		05/31/84 06/28/84 08/20/84 10/24/84	5 52 13 —	
15							
	<u>Chimp 3</u>	0.005 0.017 0.006 1.010	0.01 0.04 0.01 2.52	03/14/85	03/14/85 04/26/85 05/06/85 08/20/85	8 205 14 6	NANB
20							
	<u>Chimp 4</u>	-0.006 0.003 0.523 1.574	0.00 0.01 1.31 <u>3.93</u>	03/11/85	03/11/85 05/09/85 06/06/85 08/01/85	11 132 — —	NANB
	<u>Chimp 5</u>	-0.006 0.001 0.003 0.006	0.00 0.00 0.01 0.01	11/21/80	11/21/80 12/16/80 12/30/80 07/29 - 08/21/81	4 147 18 5	HAV
25							
	<u>Chimp 6</u>	---	---	05/25/82	—	—	HAV
		-0.005 0.001 -0.004 0.290	0.00 0.00 0.00 0.72		05/17/82 06/10/82 07/06/82 10/01/82	— — 106 10	
30							
	<u>Chimp 7</u>	-0.008 -0.004 -0.006 0.005	0.00 0.00 0.00 0.01	05/25/82	05/25/82 06/17/82 09/16/82 10/09/82	7 83 5 —	HAV

TABLE 6

CHIMPANZEE SERUM SAMPLES

(Cont'd)

		<u>OD</u>	<u>S/CO</u>	<u>INOCULATION DATE</u>	<u>BLEED DATE</u>	<u>ALT (IU/L)</u>	<u>TRANSFUSED</u>
5	<u>Chimp 8</u>	-0.007	0.00	11/21/80	11/21/80	15	HIV
		0.000	0.00		12/16/80	130	
		0.004	0.01		02/03/81	8	
		0.000	0.00		06/03 - 06/10/81	4.5	
10	<u>Chimp 9</u>	---	---	07/24/80	---	---	HIV
		0.019	0.05		08/22 - 10/10/79	---	
		---	---		03/11/81	57	
		0.015	0.04		07/01 - 08/05/81	9	
		0.008	0.02		10/01/81	6	
15	<u>Chimp 10</u>	---	---	05/12/82	---	---	HIV
		0.011	0.03		04/21 - 05/12/82	9	
		0.015	0.04		09/01 - 09/08/82	126	
		0.008	0.02		12/02/82	9	
		0.010	0.02		01/06/83	13	
20	<u>Chimp 11</u>	---	---	05/12/82	---	---	HIV
		0.000	0.00		01/06 - 05/12/82	11	
		---	---		06/23/82	100	
		-0.003	0.00		06/09 - 07/07/82	---	
		-0.003	0.00		10/28/82	9	
		-0.003	0.00		12/20/82	10	

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-140-

IV.I.3. Panel 1: Proven Infectious Sera from Chronic Human NANBH Carriers

A coded panel consisted of 22 unique samples, each one in duplicate, for a total of 44 samples. The 5 samples were from proven infectious sera from chronic NANBH carriers, infectious sera from implicated donors, and infectious sera from acute phase NANBH patients. In addition, the samples were from highly pedigreed negative controls, and other disease controls. This panel was 10 provided by Dr. H. Alter of the Department of Health and Human Services, National Institutes of Health, Bethesda, Maryland. The panel was constructed by Dr. Alter several years ago, and has been used by Dr. Alter as a qualifying panel for putative NANBH assays.

15 The entire panel was assayed twice with the ELISA assay, and the results were sent to Dr. Alter to be scored. The results of the scoring are shown in Table 7. Although the Table reports the results of only one set of duplicates, the same values were obtained for each of the 20 duplicate samples.

As shown in Table 7, 6 sera which were proven infectious in a chimpanzee model were strongly positive. The seventh infectious serum corresponded to a sample for an acute NANBH case, and was not reactive in this ELISA. 25 A sample from an implicated donor with both normal ALT levels and equivocal results in the chimpanzee studies was non-reactive in the assay. Three other serial samples from one individual with acute NANBH were also non-reactive. All samples coming from the highly pedigreed 30 negative controls, obtained from donors who had at least 10 blood donations without hepatitis implication, were non-reactive in the ELISA. Finally, four of the samples tested had previously scored as positive in putative NANBH assays developed by others, but these assays were not

confirmable. These four samples scored negatively with the HCV ELISA.

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-142-

TABLE 7  
H. ALTER'S PANEL 1:

	PANEL	1ST RESULT	2ND RESULT
5	1) PROVEN INFECTIOUS BY CHIMPANZEE TRANSMISSION		
	A. CHRONIC NANB: Post-Tx		
	JF	+	+
	EB	+	+
	PG	+	+
10	B. IMPLICATED DONORS WITH ELEVATED ALT		
	BC	+	+
	JJ	+	+
	DB	+	+
	C. ACUTE NANB: Post-Tx		
	WII	-	-
15	2) EQUIVOCALLY INFECTIOUS BY CHIMPANZEE TRANSMISSION		
	A. IMPLICATED DONOR WITH NORMAL ALT		
	CC	-	-
	3) ACUTE NANB: Post-Tx		
	JL WEEK 1	-	-
	JL WEEK 2	-	-
	JL WEEK 3	-	-
20	4) DISEASE CONTROLS		
	A. PRIMARY BILIARY CIRRHOSIS		
	EK	-	-
	B. ALCOHOLIC HEPATITIS IN RECOVERY		
	IIB	-	-
	5) PEDIGREAED NEGATIVE CONTROLS		
	DM	-	-
	DC	-	-
	LV	-	-
25	ML	-	-
	All	-	-
	6) POTENTIAL NANB "ANTIGENS"		
	JS-80-01T-0 (ISHIDA)	-	-
	ASTERIX (TREPO)	-	-
	ZURTZ (ARNOLD)	-	-
	BECASSINE (TREPO)	-	-
30			

IV.I.4. Panel 2: Donor/Recipient NANBH

The coded panel consisted of 10 unequivocal donor-recipient cases of transfusion associated NANBH, 5 with a total of 188 samples. Each case consisted of samples of some or all the donors to the recipient, and of serial samples (drawn 3, 6, and 12 months after transfusion) from the recipient. Also included was a pre-bleed, drawn from the recipient before transfusion. The 10 coded panel was provided by Dr. H. Alter, from the NIH, and the results were sent to him for scoring.

The results, which are summarized in Table 8, show that the ELISA detected antibody seroconversion in 9 of 10 cases of transfusion associated NANBH. Samples from 15 case 4 (where no seroconversion was detected), consistently reacted poorly in the ELISA. Two of the 10 recipient samples were reactive at 3 months post transfusion. At six months, 8 recipient samples were reactive; and at twelve months, with the exception of case 4, all 20 samples were reactive. In addition, at least one antibody positive donor was found in 7 out of the 10 cases, with case 10 having two positive donors. Also, in case 10, the recipient's pre-bleed was positive for HCV antibodies. The one month bleed from this recipient dropped to borderline reactive levels, while it was elevated to positive at 25 4 and 10 month bleeds. Generally, a S/CO of 0.4 is considered positive. Thus, this case may represent a prior infection of the individual with HCV.

The ALT and HBC status for all the reactive, 30 i.e., positive, samples are summarized in Table 9. As seen in the table, 1/8 donor samples was negative for the surrogate markers and reactive in the HCV antibody ELISA. On the other hand, the recipient samples (followed up to 12 months after transfusion) had either elevated ALT, 35 positive Anti-HBC, or both.

-144-

TABLE 8  
DONOR/RECIPIENT NANB PANEL

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H. ALTER DONOR/RECIPIENT NANB PANEL

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<u>CASE</u>	<u>DONOR</u>		<u>RECIPIENT</u>		<u>Post-TX</u>				<u>12 MONTHS</u>		
			<u>PREEBLEED</u>		<u>3 MONTHS</u>		<u>6 MONTHS</u>		<u>12 MONTHS</u>		
	<u>OD</u>	<u>S/CO</u>	<u>OD</u>	<u>S/CO</u>	<u>OD</u>	<u>S/CO</u>	<u>OD</u>	<u>S/CO</u>	<u>OD</u>	<u>S/CO</u>	
15	1.	---	---	.032	0.07	.112	0.26	>3.000	>6.96	>3.000	>6.96
	2.	---	---	.059	0.14	.050	0.12	1.681	3.90	>3.000	>6.96
	3.	.403	0.94	.049	0.11	.057	0.13	>3.000	>6.96	>3.000	>6.96
	4.	---	---	.065	0.15	.073	0.17	.067	0.16	.217	0.50
	5.	>3.000	>6.96	.034	0.08	.096	0.22	>3.000	>6.96	>3.000	>6.96
	6.	>3.000	>6.96	.056	0.13	1.475	3.44	>3.000	>6.96	>3.000	>6.96
20	7.	>3.000	>6.96	.034	0.08	.056	0.13	>3.000	>6.96	>3.000	>6.96
	8.	>3.000	>6.96	.061	0.14	.078	0.18	2.262	5.28	>3.000	>6.96
	9.	>3.000	>6.96	.080	0.19	.127	0.30	.055	0.13	>3.000	>6.96
	10.	>3.000	>6.96	>3.000	>6.96	.317*	0.74	>3.000**	>6.96	>3.000***	>6.96
		>3.000	>6.96								

\* 1 MONTH. \*\* 4 MONTHS. \*\*\* 10 MONTHS

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-145-

TABLE 9
ALT AND HBc STATUS FOR REACTIVE SAMPLES IN  
H. ALTER PANEL 1

		<u>Samples</u>	<u>Anti- ALT*</u>	<u>HBc**</u>	
5		<u>Donors</u>			
		Case 3	Normal	Negative	
		Case 5	Elevated	Positive	
		Case 6	Elevated	Positive	
		Case 7	Not available	Negative	
10		Case 8	Normal	Positive	
		Case 9	Elevated	Not available	
		Case 10	Normal	Positive	
		Case 10	Normal	Positive	
		<u>Recipients</u>			
15		Case 1 12 mo	6 mo Elevated	Elevated Not tested	Positive
		Case 2 12 mo	6 mo Elevated	Elevated Not tested	Negative
20		Case 3 12 mo	6 mo Elevated	Normal Not tested***	Not tested***
		Case 5 12 mo	6 mo Elevated	Elevated Not tested	Not tested
		Case 6 6 mo	3 mo Elevated	Elevated Negative	Negative
25		12 mo	Elevated	Not tested	
		Case 7 12 mo	6 mo Elevated	Elevated Negative	Negative
		Case 8 12 mo	6 mo Elevated	Normal Not tested	Positive
30		Case 9	12 mo	Elevated	Not tested
		Case 10 10 mo	4 mo Elevated	Elevated Not tested	Not tested
35		* ALT ≥45 IU/L is above normal limits. ** Anti-HBc ≤50% (competition assay) is considered positive. *** Prebleed and 3 mo samples were negative for HBc.			

-146-

IV.I.5. Determination of HCV Infection in High Risk Group Samples

Samples from high risk groups were monitored  
5 using the ELISA to determine reactivity to HCV c100-3 antigen. These samples were obtained from Dr. Gary Tegtmeier, Community Blood Bank, Kansas City. The results are summarized in Table 10.

As shown in the table, the samples with the  
10 highest reactivity are obtained from hemophiliacs (76%). In addition, samples from individuals with elevated ALT and positive for Anti-HBc, scored 51% reactive, a value which is consistent with the value expected from clinical data and NANBH prevalence in this group. The incidence of  
15 antibody to HCV was also higher in blood donors with elevated ALT alone, blood donors positive for antibodies to Hepatitis B core alone, and in blood donors rejected for reasons other than high ALT or anti-core antibody when compared to random volunteer donors.

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-147-

TABLE 10

NANBH HIGH RISK GROUP SAMPLES

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	Group	N	Distribution		% Reactive
			N	OD	
10	Elevated ALT	35	3	>3.000	11.4%
		1	0.728		
	Anti-HBc	24	5	>3.000	20.8%
	Elevated ALT, Anti-HBc	33	12	>3.000	51.5%
		1	2.768		
		1	2.324		
15		1	0.939		
		1	0.951		
		1	0.906		
	Rejected Donors	25	5	>3.000	20.0%
	Donors with History of Hepatitis	150	19	>3.000	14.7%
20		1	0.837		
		1	0.714		
		1	0.469		
	Haemophiliacs	50	31	>3.000	76.0%
		1	2.568		
		1	2.483		
25		1	2.000		
		1	1.979		
		1	1.495		
		1	1.209		
		1	0.819		

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IV.I.6 Comparative Studies Using Anti-IgG or Anti-IgM Monoclonal Antibodies, or Polyclonal Antibodies as a Second Antibody in the HCV c100-3 ELISA

5       The sensitivity of the ELISA determination which uses the anti-IgG monoclonal conjugate was compared to that obtained by using either an anti-IgM monoclonal conjugate, or by replacing both with a polyclonal antiserum reported to be both heavy and light chain  
10 specific. The following studies were performed.

IV.I.6.a. Serial Samples from Seroconverters

15       Serial samples from three cases of NANB seroconverters were studied in the HCV c100-3 ELISA assay using in the enzyme conjugate either the anti-IgG monoclonal alone, or in combination with an anti-IgM monoclonal, or using a polyclonal antiserum. The samples were provided by Dr. Cladd Stevens, N.Y. Blood Center, N.Y.C., N.Y.. The sample histories are shown in Table 11.

20       The results obtained using an anti-IgG monoclonal antibody-enzyme conjugate are shown in Table 12. The data shows that strong reactivity is initially detected in samples 1-4, 2-8, and 3-5, of cases 1, 2, and 3, respectively.

25       The results obtained using a combination of an anti-IgG monoclonal conjugate and an anti-IgM conjugate are shown in Table 13. Three different ratios of anti-IgG to anti-IgM were tested; the 1:10,000 dilution of anti-IgG was constant throughout. Dilutions tested for the anti-  
30 IgM monoclonal conjugate were 1:30,000, 1:60,000, and 1:120,000. The data shows that, in agreement with the studies with anti-IgG alone, initial strong reactivity is detected in samples 1-4, 2-8, and 3-5.

35       The results obtained with the ELISA using anti-IgG monoclonal conjugate (1:10,000 dilution), or Tago

-149-

5 polyclonal conjugate (1:80,000 dilution), or Jackson  
polyclonal conjugate (1:80,000 dilution) are shown in  
Table 14. The data indicates that initial strong reactiv-  
ity is detected in samples 1-4, 2-8, and 3-5 using all  
three configurations; the Tago polyclonal antibodies  
yielded the lowest signals.

10 The results presented above show that all three  
configurations detect reactive samples at the same time  
after the acute phase of the disease (as evidenced by the  
ALT elevation). Moreover, the results indicate that the  
sensitivity of the HCV c100-3 ELISA using anti-IgG  
monoclonal-enzyme conjugate is equal to or better than  
that obtained using the other tested configurations for  
the enzyme conjugate.  
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-150-

TABLE 11DESCRIPTION OF SAMPLES FROM CLADD STEVENS PANEL

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		Date	HBsAg	Anti-HBs	Anti-HBc	ALT	Bilirubin
<u>Case 1</u>							
10	1-1	8/5/81	1.0	91.7	12.9	40.0	-1.0
	1-2	9/2/81	1.0	121.0	15.1	274.0	1.4
	1-3	10/7/81	1.0	64.0	23.8	261.0	0.9
	1-4	11/19/81	1.0	67.3	33.8	75.0	0.9
	1-5	12/15/81	1.0	50.5	27.6	71.0	1.0
<u>Case 2</u>							
15	2-1	10/19/81	1.0	1.0	116.2	17.0	-1.0
	2-2	11/17/81	1.0	0.8	89.5	46.0	1.1
	2-3	12/02/81	1.0	1.2	78.3	63.0	1.4
	2-4	12/14/81	1.0	0.9	90.6	152.0	1.4
	2-5	12/23/81	1.0	0.8	93.6	624.0	1.7
	2-6	1/20/82	1.0	0.8	92.9	66.0	1.5
	2-7	2/15/82	1.0	0.8	86.7	70.0	1.3
	2-8	3/17/82	1.0	0.9	69.8	24.0	-1.0
	2-9	4/21/82	1.0	0.9	67.1	53.0	1.5
	2-10	5/19/82	1.0	0.5	74.8	95.0	1.6
	2-11	6/14/82	1.0	0.8	82.9	37.0	-1.0
<u>Case 3</u>							
20	3-1	4/7/81	1.0	1.2	88.4	13.0	-1.0
	3-2	5/12/81	1.0	1.1	126.2	236.0	0.4
	3-3	5/30/81	1.0	0.7	99.9	471.0	0.2
	3-4	6/9/81	1.0	1.2	110.8	315.0	0.4
	3-5	7/6/81	1.0	1.1	89.9	273.0	0.4
	3-6	8/10/81	1.0	1.0	118.2	158.0	0.4
	3-7	9/8/81	1.0	1.0	112.3	84.0	0.3
	3-8	10/14/81	1.0	0.9	102.5	180.0	0.5
	3-9	11/11/81	1.0	1.0	84.6	154.0	0.3
25							
30							
35							

-151-

TABLE 12

## ELISA RESULTS OBTAINED USING AN ANTI-IgG MONOCLONAL CONJUGATE

5

<u>SAMPLE</u>	<u>DATE</u>	<u>ALT</u>	<u>DD</u>	<u>S/CO</u>
NEG CONTROL			.076	
CUTOFF			.476	
PC (1:128)			1.390	

1.0

CASE #1

1-1	08/05/81	40.0	.178	.37
1-2	09/02/81	274.0	.154	.32
1-3	10/07/81	261.0	.129	.27
1-4	11/19/81	75.0	.937	1.97
1-5	12/15/81	71.0	>3,000	>6,30

15

CASE #2

20

2-1	10/19/81	17.0	.058	0.12
2-2	11/17/81	46.0	.050	0.11
2-3	12/02/81	63.0	.047	0.10
2-4	12/14/81	152.0	.059	0.12
2-5	12/23/81	624.0	.070	0.15
2-6	01/20/82	66.0	.051	0.11
2-7	02/15/82	70.0	.139	0.29
2-8	03/17/82	24.0	1.867	3.92
2-9	04/21/82	53.0	>3.000	>6.30
2-10	05/19/82	95.0	>3.000	>6.30
2-11	06/14/82	37.0	>3.000	>6.30

25

Case #3

3-1	04/07/81	13.0	.090	.19
3-2	05/12/81	236.0	.064	.13
3-3	05/30/81	471.0	.079	.17
3-4	06/09/81	315.0	.211	.44
3-5	07/06/81	273.0	1.707	3.59
3-6	08/10/81	158.0	>3.000	>6.30
3-7	09/08/81	84.0	>3.000	>6.30
3-8	10/14/81	180.0	>3.000	>6.30
3-9	11/11/81	154.0	>3.000	>6.30

-152-

TABLE 13ELISA RESULTS OBTAINED USING ANTI-IgG and ANTI-IgMMONOCLONAL CONJUGATE

5

	<u>SAMPLE</u>	<u>DATE</u>	<u>ALT</u>	NANB ELISAs			
				MONOCLONALS		MONOCLONALS	
				IgG 1:10K	IgG 1:10K	IgG 1:10K	IgG 1:10K
				IgM 1:30K	IgM 1:60K	IgM 1:120K	IgM 1:120K
				<u>OD</u>	<u>S/CO</u>	<u>OD</u>	<u>S/CO</u>
10	NEG CONTROL			.100		.080	.079
	CUTOFF						
	PC (1:128)			1.083		1.328	1.197
	<u>CASE #1</u>						
15	1-1	08/05/81	40	.173		.162	.070
	1-2	09/02/81	274	.194		.141	.079
	1-3	10/07/81	261	.162		.129	.063
	1-4	11/19/81	75	.812		.85	.709
	1-5	12/15/81	71	>3.00		>3.00	>3.00
	<u>Case #2</u>						
20	2-1	10/19/81	17	.442		.045	.085
	2-2	11/17/81	46	.102		.029	.030
	2-3	12/02/81	63	.059		.036	.027
	2-4	12/14/81	152	.065		.041	.025
	2-5	12/23/81	624	.082		.033	.032
	2-6	01/20/82	66	.102		.042	.027
	2-7	02/15/82	70	.188		.068	.096
25	2-8	03/17/82	24	1.728		1.668	1.541
	2-9	04/21/82	53	>3.00		2.443	>3.00
	2-10	05/19/82	95	>3.00		>3.00	>3.00
	2-11	06/14/82	37	>3.00		>3.00	>3.00
	<u>Case #3</u>						
30	3-1	04/07/81	13	.193		.076	.049
	3-2	05/12/81	236	.201		.051	.038
	3-3	05/30/81	471	.132		.067	.052
	3-4	06/09/81	315	.175		.155	.140
	3-5	07/06/81	273	1.335		1.238	1.260
	3-6	08/10/81	158	>3.00		>3.00	>3.00
	3-7	09/08/81	84	>3.00		>3.00	>3.00
35	3-8	10/14/81	180	>3.00		>3.00	>3.00
	3-9	11/11/81	154	>3.00		>3.00	>3.00

TABLE 14

ELISA RESULTS OBTAINED USING POLYCLONAL CONJUGATES

	SAMPLE	DATE	ALT	NANB ELISAs				JACKSON	
				MONOCLONAL		TAGO		1:80K	
				1:10K	S/CO	1:80K	S/CO	1:80K	S/CO
5	NEG CONTROL			.076		.045		.154	
10	CUTOFF			.476		.545		.654	
	PC (1:128)			<u>1.390</u>		<u>.727</u>		<u>2.154</u>	
	<u>CASE #1</u>								
15	1-1	08/05/81	40	.178	.37	.067	.12	.153	.23
	1-2	09/02/81	274	.154	.32	.097	.18	.225	.34
	1-3	10/07/81	261	.129	.27	.026	.05	.167	.26
	1-4	11/19/81	75	.937	1.97	.324	.60	.793	1.21
	1-5	12/15/81	71	>3.00	>6.30	1.778	3.27	>3.00	>4.59
	<u>CASE #2</u>								
20	2-1	10/19/81	17	.058	.12	.023	.04	.052	.08
	2-2	11/17/81	46	.050	.11	.018	.03	.058	.09
	2-3	12/02/81	63	.047	.10	.020	.04	.060	.09
	2-4	12/14/81	152	.059	.12	.025	.05	.054	.08
	2-5	12/23/81	624	.070	.15	.026	.05	.074	.11
	2-6	01/20/82	66	.051	.11	.018	.03	.058	.09
	2-7	02/15/82	70	.139	.29	.037	.07	.146	.22
	2-8	03/17/82	24	1.867	3.92	.355	.65	1.429	2.19
	2-9	04/21/82	53	>3.00	>6.30	.748	1.37	>3.00	>4.59
	2-10	05/19/82	95	>3.00	>6.30	1.025	1.88	>3.00	>4.59
25	2-11	06/14/82	37	>3.00	>6.30	.917	1.68	>3.00	>4.59
	<u>CASE #3</u>								
30	3-1	04/07/81	13	.090	.19	.049	.09	.138	.21
	3-2	05/12/81	236	.064	.13	.040	.07	.094	.14
	3-3	05/30/81	471	.079	.17	.045	.08	.144	.22
	3-4	06/09/81	315	.211	.44	.085	.16	.275	.42
	3-5	07/06/81	273	1.707	3.59	.272	.50	1.773	2.71
	3-6	08/10/81	158	>3.00	>6.30	1.347	2.47	>3.00	>4.59
	3-7	09/08/81	84	>3.00	>6.30	2.294	4.21	>3.00	>4.59
	3-8	10/14/81	180	>3.00	>6.30	>3.00	>5.50	>3.00	>4.59
	3-9	11/11/81	154	>3.00	>6.30	>3.00	>5.50	>3.00	>4.59

IV.I.6.b. Samples from Random Blood Donors

Samples from random blood donors (See Section IV.I.1.) were screened for HCV infection using the HCV c100-3 ELISA, in which the antibody-enzyme conjugate was either an anti-IgG monoclonal conjugate, or a polyclonal conjugate. The total number of samples screened were 1077 and 1056, for the polyclonal conjugate and the monoclonal conjugate, respectively. A summary of the results of the screening is shown in Table 15, and the sample distributions are shown in the histogram in Fig. 44.

The calculation of the average and standard deviation was performed excluding samples that gave a signal over 1.5, i.e., 1073 OD values were used for the calculations utilizing the polyclonal conjugate, and 1051 for the anti-IgG monoclonal conjugate. As seen in Table 15, when the polyclonal conjugate was used, the average was shifted from 0.0493 to 0.0931, and the standard deviation was increased from 0.074 to 0.0933. Moreover, the results also show that if the criteria of  $\bar{x} + 5SD$  is employed to define the assay cutoff, the polyclonal-enzyme conjugate configuration in the ELISA requires a higher cutoff value. This indicates a reduced assay specificity as compared to the monoclonal system. In addition, as depicted in the histogram in Fig. 44, a greater separation of results between negative and positive distributions occurs when random blood donors are screened in an ELISA using the anti-IgG monoclonal conjugate as compared to the assay using a commercial polyclonal label.

-155-

TABLE 15COMPARISON OF TWO ELISA CONFIGURATIONS IN  
TESTING SAMPLES FROM RANDOM BLOOD DONORS

10	<u>CONJUGATE</u>	<u>POLYCLONAL</u> (Jackson)	<u>ANTI-IgG MONOCLONAL</u>
15	Number of samples	1073	1051
	Average ( $\bar{x}$ )	0.0931	0.04926
	Standard deviation (SD)	0.0933	0.07427
	5 SD	0.4666	0.3714
	CUT-OFF (5 SD + $\bar{x}$ )	0.5596	0.4206

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-156-

**IV.J. Detection of HCV Seroconversion in NANBH Patients from a Variety of Geographical Locations**

Sera from patients who were suspected to have  
 5 NANBH based upon elevated ALT levels, and who were  
 negative in HAV and HBV tests were screened using the RIA  
 essentially as described in Section IV.D., except that the  
 HCV C100-3 antigen was used as the screening antigen in  
 the microtiter plates. As seen from the results presented  
 10 in Table 16, the RIA detected positive samples in a high  
 percentage of the cases.

**Table 16**  
**Seroconversion Frequencies for Anti-c100-3**  
 15 **Among NANBH Patients in Different Countries**

	<u>Country</u>	<u>The Netherlands</u>	<u>Italy</u>	<u>Japan</u>
	No.			
20	Examined	5	36	26
	No.			
	Positive	3	29	19
25	%			
	Positive	60	80	73

**IV.K. Detection of HCV Seroconversion in Patients with "Community Acquired" NANBH**

Sera which was obtained from 100 patients with  
 NANBH, for whom there was no obvious transmission route  
 (i.e., no transfusions, i.v. drug use, promiscuity, etc.  
 were identified as risk factors), was provided by Dr. M.  
 35 Alter of the Center for Disease Control, and Dr. J.

Dienstag of Harvard University. These samples were screened using an RIA essentially as described in Section IV.D., except that the HCV c100-3 antigen was used as the screening antigen attached to the microtiter plates. The 5 results showed that of the 100 serum samples, 55 contained antibodies that reacted immunologically with the HCV c100-3 antigen.

The results described above suggest that "Community Acquired" NANBH is also caused by HCV. 10 Moreover, since it has been demonstrated herein that HCV is related to Flaviviruses, most of which are transmitted by arthropods, it is suggestive that HCV transmission in the "Community Acquired" cases also results from arthropod transmission.

15 IV.L. Comparison of Incidence of HCV Antibodies and Surrogate Markers in Donors Implicated in NANBH Transmission

A prospective study was carried out to determine 20 whether recipients of blood from suspected NANBH positive donors, who developed NANBH, seroconverted to anti-HCV- antibody positive. The blood donors were tested for the surrogate marker abnormalities which are currently used as markers for NANBH infection, i.e., elevated ALT levels, 25 and the presence of anti-core antibody. In addition, the donors were also tested for the presence of anti-HCV antibodies. The determination of the presence of anti-HCV antibodies was determined using a radioimmunoassay as described in Section IV.K. The results of the study are 30 presented in Table 17, which shows: the patient number (column 1); the presence of anti-HCV antibodies in patient serum (column 2); the number of donations received by the patient, with each donation being from a different donor (column 3); the presence of anti-HCV antibodies in donor 35 serum (column 4); and the surrogate abnormality of the

-158-

donor (column 5) (NT or -- means not tested) (ALT is elevated transaminase, and ANTI-HBc is anti-core antibody).

The results in Table 17 demonstrate that the HCV antibody test is more accurate in detecting infected blood donors than are the surrogate marker tests. Nine out of ten patients who developed NANBH symptoms tested positive for anti-HCV antibody seroconversion. Of the 11 suspected donors, (patient 6 received donations from two different individuals suspected of being NANBH carriers), 9 were positive for anti-HCV antibodies, and 1 was borderline positive, and therefore equivocal (donor for patient 1). In contrast, using the elevated ALT test 6 of the ten donors tested negative, and using the anticore-antibody test 5 of the ten donors tested negative. Of greater consequence, though, in three cases (donors to patients 8, 9, and 10) the ALT test and the ANTI-HBc test yielded inconsistent results.

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-159-

Table 17

DEVELOPMENT OF ANTI-HCV ANTIBODIES IN PATIENTS  
RECEIVING BLOOD FROM DONORS SUSPECTED OF BEING NANBH CARRIERS

Patient	Anti-HCV Seroconversion in Patient	No. of Donations/Donors	Anti-HCV Positive Donor	Surrogate Abnormality Alt Anti-HB
1	yes	18	equiv	no no
2	yes	18	yes	NT yes
3	yes	13	yes	no no
4	no	18	no	-- --
5	yes	16	yes	yes yes
6	yes	11	yes(2)	no no
7	yes	15	yes	yes yes
8	yes	20	yes	NT no
9	yes	5	yes	no yes
10	yes	15	yes	no yes

\*Same donor as anti-NANBV Positive.

IV.M. Amplification for Cloning of HCV cDNA Sequences Utilizing the PCR and Primers Derived from Conserved Regions of Flavivirus Genomic Sequences

The results presented supra., which suggest that HCV is a flavivirus or flavi-like virus, allows a strategy for cloning uncharacterized HCV cDNA sequences utilizing the PCR technique, and primers derived from the regions encoding conserved amino acid sequences in flaviviruses. Generally, one of the primers is derived from a defined HCV genomic sequence, and the other primer which flanks a region of unsequenced HCV polynucleotide is derived from a conserved region of the flavivirus genome. The flavivirus genomes are known to contain conserved sequences within the NS1, and E polypeptides, which are encoded in the 5'-region of the flavivirus genome. Corresponding sequences encoding these regions lie upstream of the HCV cDNA sequence shown in Fig. 26. Thus, to isolate cDNA sequences derived from this region of the HCV genome, upstream primers are designed which are derived from the conserved sequences within these flavivirus polypeptides. The downstream primers are derived from an upstream end of the known portion of the HCV cDNA.

Because of the degeneracy of the code, it is probable that there will be mismatches between the flavivirus probes and the corresponding HCV genomic sequence. Therefore a strategy which is similar to the one described by Lee (1988) is used. The Lee procedure utilizes mixed oligonucleotide primers complementary to the reverse translation products of an amino acid sequence; the sequences in the mixed primers takes into account every codon degeneracy for the conserved amino acid sequence.

Three sets of primer mixes are generated, based on the amino acid homologies found in several flaviviruses, including Dengue-2,4 (D-2,4), Japanese

-161-

Encephalitis Virus (JEV), Yellow Fever (YF), and West Nile Virus (WN). The primer mixture derived from the most upstream conserved sequence (5'-1), is based upon the amino acid sequence gly-trp-gly, which is part of the 5 conserved sequence asp-arg-gly-trp-gly-aspN found in the E protein of D-2, JEV, YF, and WN. The next primer mixture (5'-2) is based upon a downstream conserved sequence in E protein, phe-asp-gly-asp-ser-tyr-ileu-phe-gly-asp-ser-tyr-ileu, and is derived from phe-gly-asp; the conserved 10 sequence is present in D-2, JEV, YF, and WN. The third primer mixture (5'-3), is based on the amino acid sequence arg-ser-cys, which is part of the conserved sequence cys-cys-arg-ser-cys in the NS1 protein of D-2, D-4, JEV, YF, and WN. The individual primers which form the mixture in 15 5'-3 are shown in Fig. 45. In addition to the varied sequences derived from conserved region, each primer in each mixture also contains a constant region at the 5'-end which contains a sequence encoding sites for restriction enzymes, HindIII, MboI, and EcoRI.

20 The downstream primer, ssc5h20A, is derived from a nucleotide sequence in clone 5h, which contains HCV cDNA with sequences with overlap those in clones 14i and 11b. The sequence of ssc5h20A is

25 5' GTA ATA TGG TGA CAG AGT CA 3'.

An alternative primer, ssc5h34A, may also be used. This 30 primer is derived from a sequence in clone 5h, and in addition contains nucleotides at the 5'-end which create a restriction enzyme site, thus facilitating cloning. The sequence of ssc5h34A is

5' GAT CTC TAG AGA AAT CAA TAT GGT GAC AGA GTC A 3'.

-162-

The PCR reaction, which was initially described by Saiki et al. (1986), is carried out essentially as described in Lee et al. (1988), except that the template for the cDNA is RNA isolated from HCV infected chimpanzee liver, as described in Section IV.C.2., or from viral particles isolated from HCV infected chimpanzee serum, as described in Section IV.A.1. In addition, the annealing conditions are less stringent in the first round of amplification (0.6M NaCl, and 25°C), since the part of the primer which will anneal to the HCV sequence is only 9 nucleotides, and there could be mismatches. Moreover, if ssc5h34A is used, the additional sequences not derived from the HCV genome tend to destabilize the primer-template hybrid. After the first round of amplification, the annealing conditions can be more stringent (0.066M NaCl, and 32°C-37°C), since the amplified sequences now contain regions which are complementary to, or duplicates of the primers. In addition, the first 10 cycles of amplification are run with Klenow enzyme I, under appropriate PCR conditions for that enzyme. After the completion of these cycles, the samples are extracted, and run with Taq polymerase, according to kit directions, as furnished by Cetus/Perkin-Elmer.

After the amplification, the amplified HCV cDNA sequences are detected by hybridization using a probe derived from clone 5h. This probe is derived from sequences upstream of those used to derive the primer, and does not overlap the sequences of the clone 5h derived primers. The sequence of the probe is

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5' CCC AGC GGC GTA CGC GCT GGA CAC GGA GGT GGC CGC GTC  
GTG TGG CGG TGT TGT TCT CGT CGG GTT GAT GGC GC 3'.

-163-

IV.N.1. Creation of HCV cDNA Library From Liver of a Chimpanzee with Infectious NANBH

An HCV cDNA library was created from liver from the chimpanzee from which the HCV cDNA library in Section 5 IV.A.1. was created. The technique for creating the library was similar to that in Section IV.A.24, except for this different source of the RNA, and that a primer based on the sequence of HCV cDNA in clone 11b was used. The sequence of the primer was

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5' CTG GCT TGA AGA ATC 3'.

IV.N.2. Isolation and Nucleotide Sequence of Overlapping HCV cDNA in Clone k9-1 to cDNA in Clone 11b

15 Clone k9-1 was isolated from the HCV cDNA library created from the liver of an NANBH infected chimpanzee, as described in Section IV.A.25. The library was screened for clones which overlap the sequence in clone 11b, by using a clone which overlaps clone 11b at 20 the 5'-terminus, clone 11e. The sequence of clone 11b is shown in Fig. 23. Positive clones were isolated with a frequency of 1 in 500,000. One isolated clone, k9-1, was subjected to further study. The overlapping nature of the 25 HCV cDNA in clone k9-1 to the 5'-end of the HCV-cDNA sequence in Fig. 26 was confirmed by probing the clone with clone Alex46; this latter clone contains an HCV cDNA sequence of 30 base pairs which corresponds to those base pairs at the 5'terminus of the HCV cDNA in clone 14i, described supra.

30 The nucleotide sequence of the HCV cDNA isolated from clone k9-1 was determined using the techniques described supra. The sequence of the HCV cDNA in clone k9-1, the overlap with the HCV cDNA in Fig. 26, and the amino acids encoded therein are shown in Fig. 46.

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-164-

The HCV cDNA sequence in clone k9-1 has been aligned with those of the clones described in Section IV.A.19. to create a composite HCV cDNA sequence, with the k9-1 sequence being placed upstream of the sequence shown 5 in Fig. 32. The composite HCV cDNA which includes the k9-1 sequence, and the amino acids encoded therein, is shown in Fig. 47.

The sequence of the amino acids encoded in the 5'-region of HCV cDNA shown in Fig. 47 has been compared 10 with the corresponding region of one of the strains of Dengue virus, described supra., with respect to the profile of regions of hydrophobicity and hydrophilicity. This comparison showed that the polypeptides from HCV and 15 Dengue encoded in this region, which corresponds to the region encoding NS1 (or a portion thereof), have a similar hydrophobic/hydrophilic profile.

The information provided infra. allows the identification of HCV strains. The isolation and characterization of other HCV strains may be accomplished 20 by isolating the nucleic acids from body components which contain viral particles, creating cDNA libraries using polynucleotide probes based on the HCV cDNA probes described infra., screening the libraries for clones containing HCV cDNA sequences described infra., and 25 comparing the HCV cDNAs from the new isolates with the cDNAs described infra. The polypeptides encoded therein, or in the viral genome, may be monitored for immunological cross-reactivity utilizing the polypeptides and antibodies described supra. Strains which fit within the parameters 30 of HCV, as described in the Definitions section, supra., are readily identifiable. Other methods for identifying HCV strains will be obvious to those of skill in the art, based upon the information provided herein.

Industrial Applicability

The invention, in the various manifestations disclosed herein, has many industrial uses, some of which are the following. The HCV cDNAs may be used for the 5 design of probes for the detection of HCV nucleic acids in samples. The probes derived from the cDNAs may be used to detect HCV nucleic acids in, for example, chemical synthetic reactions. They may also be used in screening programs for anti-viral agents, to determine the effect of 10 the agents in inhibiting viral replication in cell culture systems, and animal model systems. The HCV polynucleotide probes are also useful in detecting viral nucleic acids in humans, and thus, may serve as a basis for diagnosis of HCV infections in humans.

15 In addition to the above, the cDNAs provided herein provide information and a means for synthesizing polypeptides containing epitopes of HCV. These polypeptides are useful in detecting antibodies to HCV antigens. A series of immunoassays for HCV infection, 20 based on recombinant polypeptides containing HCV epitopes are described herein, and will find commercial use in diagnosing HCV induced NANBH, in screening blood bank donors for HCV-caused infectious hepatitis, and also for detecting contaminated blood from infectious blood donors. 25 The viral antigens will also have utility in monitoring the efficacy of anti-viral agents in animal model systems. In addition, the polypeptides derived from the HCV cDNAs disclosed herein will have utility as vaccines for treatment of HCV infections.

30 The polypeptides derived from the HCV cDNAs, besides the above stated uses, are also useful for raising anti-HCV antibodies. Thus, they may be used in anti-HCV vaccines. However, the antibodies produced as a result of immunization with the HCV polypeptides are also useful in 35 detecting the presence of viral antigens in samples. Thus,

they may be used to assay the production of HCV polypeptides in chemical systems. The anti-HCV antibodies may also be used to monitor the efficacy of anti-viral agents in screening programs where these agents are tested  
5 in tissue culture systems. They may also be used for passive immunotherapy, and to diagnose HCV caused NANBH by allowing the detection of viral antigen(s) in both blood donors and recipients. Another important use for anti-HCV antibodies is in affinity chromatography for the  
10 purification of virus and viral polypeptides. The purified virus and viral polypeptide preparations may be used in vaccines. However, the purified virus may also be useful for the development of cell culture systems in which HCV replicates.

15 Cell culture systems containing HCV infected cells will have many uses. They can be used for the relatively large scale production of HCV, which is normally a low titer virus. These systems will also be useful for an elucidation of the molecular biology of the  
20 virus, and lead to the development of anti-viral agents. The cell culture systems will also be useful in screening for the efficacy of antiviral agents. In addition, HCV permissive cell culture systems are useful for the production of attenuated strains of HCV.

25 For convenience, the anti-HCV antibodies and HCV polypeptides, whether natural or recombinant, may be packaged into kits.

The method used for isolating HCV cDNA, which is comprised of preparing a cDNA library derived from  
30 infected tissue of an individual, in an expression vector, and selecting clones which produce the expression products which react immunologically with antibodies in antibody-containing body components from other infected individuals and not from non-infected individuals, may also be  
35 applicable to the isolation of cDNAs derived from other

-167-

heretofore uncharacterized disease-associated agents which  
are comprised of a genomic component. This, in turn,  
could lead to isolation and characterization of these  
agents, and to diagnostic reagents and vaccines for these  
other disease-associated agents.

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-168-

CLAIMS

1. A purified HCV polynucleotide.

5 2. A recombinant HCV polynucleotide.

3. A recombinant polynucleotide comprising a sequence derived from an HCV genome or from HCV cDNA.

10 4. A recombinant polynucleotide encoding an epitope of HCV.

5. A recombinant vector containing the polynucleotide of claim 2, or claim 3, or claim 4.

15 6. A host cell transformed with the vector of claim 5.

20 7. A recombinant expression system comprising an open reading frame (ORF) of DNA derived from an HCV genome or from HCV cDNA, wherein the ORF is operably linked to a control sequence compatible with a desired host.

25 8. A cell transformed with the recombinant expression system of claim 7.

9. A polypeptide produced by the cell of claim 8.

30 10. Purified HCV.

11. A preparation of polypeptides from the HCV of claim 10.

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-169-

12. A purified HCV polypeptide.

13. A purified polypeptide comprising an epitope which is immunologically identifiable with an 5 epitope contained in HCV.

14. A recombinant HCV polypeptide.

15. A recombinant polypeptide comprised of a 10 sequence derived from an HCV genome or from HCV cDNA.

16. A recombinant polypeptide comprised of an HCV epitope.

17. A fusion polypeptide comprised of an HCV 15 polypeptide.

18. A monoclonal antibody directed against an HCV epitope.

19. A purified preparation of polyclonal 20 antibodies directed against HCV.

20. A particle which is immunogenic against HCV 25 infection comprising a non-HCV polypeptide having an amino acid sequence capable of forming a particle when said sequence is produced in a eukaryotic host, and an HCV epitope.

30. A polynucleotide probe for HCV.

35. A kit for analyzing samples for the presence of polynucleotides derived from HCV comprising a polynucleotide probe containing a nucleotide sequence from

HCV of about 8 or more nucleotides, in a suitable container.

23. A kit for analyzing samples for the  
5 presence of an HCV antigen comprising an antibody directed against the HCV antigen to be detected, in a suitable container.

24. A kit for analyzing samples for the  
10 presence of an antibodies directed against an HCV antigen comprising a polypeptide containing an HCV epitope present in the HCV antigen, in a suitable container.

25. A polypeptide comprised of an HCV epitope,  
15 attached to a solid substrate.

26. An antibody to an HCV epitope, attached to a solid substrate.

20 27. A method for producing a polypeptide containing an HCV epitope comprising incubating host cells transformed with an expression vector containing a sequence encoding a polypeptide containing an HCV epitope under conditions which allow expression of said  
25 polypeptide.

28. A polypeptide containing an HCV epitope produced by the method of claim 27.

30 29. A method for detecting HCV nucleic acids in a sample comprising:

(a) reacting nucleic acids of the sample with a probe for an HCV polynucleotide under conditions which allow the formation of a polynucleotide duplex between the  
35 probe and the HCV nucleic acid from the sample; and

(b) detecting a polynucleotide duplex which contains the probe.

30. An immunoassay for detecting an HCV antigen comprising:

5 (a) incubating a sample suspected of containing an HCV antigen with a probe antibody directed against the HCV antigen to be detected under conditions which allow the formation of an antigen-antibody complex; and

10 (b) detecting an antigen-antibody complex containing the probe antibody.

31. An immunoassay for detecting antibodies directed against an HCV antigen comprising:

15 (a) incubating a sample suspected of containing anti-HCV antibodies with a probe polypeptide which contains an epitope of the HCV, under conditions which allow the formation of an antibody-antigen complex; and

20 (b) detecting the antibody-antigen complex containing the probe antigen.

32. A vaccine for treatment of HCV infection comprising an immunogenic polypeptide containing an HCV epitope wherein the immunogenic polypeptide is present in a pharmacologically effective dose in a pharmaceutically acceptable excipient.

33. A vaccine for treatment of HCV infection comprising inactivated HCV in a pharmacologically effective dose in a pharmaceutically acceptable excipient.

34. A vaccine for treatment of HCV infection comprising attenuated HCV in a pharmacologically effective dose in a pharmaceutically acceptable excipient.

-172-

35. A tissue culture grown cell infected with HCV.

36. The HCV infected cell of claim 35, wherein  
5 the cell is of a human macrophage cell line, or is of a hepatocyte cell line, or is of a mosquito cell line, or is of a tick cell line, or is of a mouse macrophage cell line, or is an embryonic cell.

10 37. The HCV infected cell of claim 35, wherein  
the cell is of a cell line derived from liver of an HCV infected individual.

15 38. A method for producing antibodies to HCV comprising administering to an individual an isolated immunogenic polypeptide containing an HCV epitope in an amount sufficient to produce an immune response.

20 39. A method for producing antibodies to HCV comprising administering to an individual the polypeptide preparation of claim 11, wherein the preparation contains at least 1 immunogenic polypeptide, and the administering is of an amount sufficient to produce an immune response.

25 40. A method for isolating cDNA derived from the genome of an unidentified infectious agent, comprising:

30 (a) providing host cells transformed with expression vectors containing a cDNA library prepared from nucleic acids isolated from tissue infected with the agent and growing said host cells under conditions which allow expression of polypeptide(s) encoded in the cDNA;

35 (b) interacting the expression products of the cDNA with an antibody containing body component of an individual infected with said infectious agent under

-173-

conditions which allow an immunoreaction, and detecting antibody-antigen complexes formed as a result of the interacting;

5 (c) growing host cells which express polypeptides that form antibody-antigen complexes in step  
(b) under conditions which allow their growth as individual clones and isolating said clones;

10 (d) growing cells from the clones of (c) under conditions which allow expression of polypeptide(s) encoded within the cDNA, and interacting the expression products with antibody containing body components of individuals other than the individual in step (a) who are infected with the infectious agent and with control individuals uninfected with the agent, and detecting 15 antibody-antigen complexes formed as a result of the interacting;

15 (e) growing host cells which express polypeptides that form antibody-antigen complexes with antibody containing body components of infected 20 individuals and individuals suspected of being infected, and not with said components of control individuals, under conditions which allow their growth as individual clones and isolating said clones; and

25 (f) isolating the cDNA from the host cell clones of (e).

**FIG. 1** Translation of DNA 5-1-1

1 AlaSerCysLeuAsnCysSerAlaSerIleIleProAspArgGluValLeuTyrArgGlu  
 GGCCTCCTGCTTGAAC TGCTCGCGAGCATCACCTGACAGGGAA GTCCCTCTACCGAGA  
 CCGGAGGACGA ACTTGACGAGCCGCTCGTAGTATGGACTGTCCCTTCAGGAGATGGCTCT  
 61 PheAspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeu  
 GTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCT  
 CAAGCTACTCTACCTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTTCCCTACTACGA  
 121 AlaGluGlnPheLysGlnLysAlaLeuGlyLeu  
 CGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCCTCC  
 GCGGCTCGTCAAGTTCGTCTCCGGGAGCCGGAGG

**FIG. 3** Translation of DNA 5-1-1, 81, 91&1-2

1 GlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIleProAsp  
 CTGGCTGCGTGGTCATAGTGGCAGGGTCGTCTGTCCGGGAAGCCGGCAATCATACCTG  
 GACCGACGCACCAGTATCACCGTCCCAGCAGAACAGGCCCTCGGCCGTTAGTATGGAC  
 T  
 61 ArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeuProTyr  
 ACAGGGAA GTCCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGT  
 TGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCGTCTCACGAGAGTCGTGAATGGCA  
 A  
 121 IleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeuGln  
 ACATCGAGCAAGGGATGATGCTCGCGAGCAGTTCAAGCAGAACAGGCCCTCGGCCCTCGC  
 TGTAGCTCGTCCCTACTACGAGCGGCTCGTCAAGTCGTCTCCGGGAGCCGGAGGACG  
 181 ThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLysLeu  
 AGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCGCTGTCCAGACCAACTGGAAAAAC  
 TCTGGCGCAGGGCAGTCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTTTTG  
 241 GluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAlaGly  
 TCGAGACCTCTGGCGAAGCATATGTGGAACTTCATCAGTGGGATAACAATACTTGGCGG  
 AGCTCTGGAAGACCCGCTCGTATACACCTTGAAGTAGTCACCCATTGTTATGAACCGCC  
 301 LeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAlaVal  
 GCTTGTCAACGCTGCCTGGTAACCCGCCATTGCTTACAGTGGCTTTACAGCTGCTG  
 CGAACAGTTGCGACGGACCATTGGGGCGGTAAAGTAACCGAAATGTCGACGAC  
 361 ThrSerProLeuThrThrSerGln  
 TCACCAGCCCACCAACCAGCCAAA  
 AGTGGTCGGGTGATTGGTGATCGGTT

2 / 63

2  
EIG

81 324 ctgtcaccaaggcccactaacccacttagccaaa

3 / 63

**FIG. 4** Translation of DNA 81

1 SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet  
 GTCCGGGAAGCCGGCAATCATACCTGACAGGGAAAGTCCTCTACCGAGAGTCGATGAGAT  
 CAGGCCCTCGGCCGTTAGTATGGACTGTCCCTCAGGAGATGGCTCTCAAGCTACTCTA  
  
 61 GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe  
 GGAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTGCCGAGCAGTT  
 CCTTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTCCCTACTACGAGCAGCTCGTCAA  
  
 121 LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro  
 CAAGCAGAAGGCCCTCGGCCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATGCC  
 GTTCGTCTCCGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGG  
  
 181 AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe  
 TGCTGCCAGACCAACTGGCAAAAACTCGAGACCTCTGGCGAAGCATATGTGGAACCT  
 ACGACAGGTCTGGTGACCGTTTGAGCTCTGGAAGAACCGCTTCGTATAACACCTTGAA  
  
 241 IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla  
 CATCAGTGGGATACAATACTTGGCGGCTTGTCAACGCTGCCTGGTAACCCGCCATTGC  
 GTAGTCACCCATGTTATGAACCGCCGAACAGTTGCGACGGACCATTGGGGCGGTAAACG  
  
 301 SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
 TTCAATTGATGGCTTTACAGCTGCTGTCACCAGCCCCTAACCAACTAGCCAAA  
 AAGTAACCTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTATCGGTTT

**FIG. 5** Translation of DNA 36

1 AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla  
 GATGCCCACTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTCCTTACCTGGTAGCG  
 CTACGGGTGAAAGATAGGGCTGTTCTACCCCTCTGGAAAGGAATGGACCATCGC  
  
 61 TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProSerTrpAspGlnMetTrp  
 TACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCATCGTGGGACAGATGTGG  
 ATGGTTCGGTGGCACACGCGATCCGAGTTCGGGAGGGGGTAGCACCTGGTCTACACC  
  
 121 LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu  
 AAGTGTGATTGCGCTCAAGCCCACCCCTCCATGGGCCAACACCCCTGCTATACAGACTG  
 TTCACAAACTAACGGAGTTGGTGGGAGGTACCGGTTGTGGGACGATATGTCTGAC  
  
 181 GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys  
 GCGCCTGTCAGAATGAAATACCCCTGACGCACCCAGTCACCAAATACATCATGACATGC  
 CCGCGACAAGTCTACTTACTGGGACTGCGTGGTCAGTGGTTATGTAGTACTGTACG  
  
 241 MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla  
 ATGTCGGCCGACCTGGAGGTGCGTACGAGCACCTGGGTGCTCGTGGCGGCGTCCTGGCT  
 TACAGCCGGCTGGACCTCCAGCAGTGCTGGACCCACGAGCAACCGCCGCAGGACCGA  
  
 301 AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu  
 GCTTGGCCGCGTATTGCGCTGTCACACAGGCTGCGTGGTCAGTGGGCAGGGTCGTCTTG  
 CGAAACCGGCGCATAACGGACAGTTGTCGACGCACCGAGTACCCGTCCAGCAGAAC  
  
 -----Overlap with 81-----  
 361 SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArg  
 TCCGGGAAGCCGGCAATCATACCTGACAGGGAAAGTCCTCTACCGAG  
 AGGCCCTCGGCCGTTAGTATGGACTGTCCCTCAGGAGATGGCTC

4 / 63

**FIG. 6** Combined ORF of DNAs 36 & 81

1 AspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAla  
 1 GATGCCACTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCG  
 CTACGGGTGAAAGATAGGGTCTGTTCGTCTACCCCTCTGGAAAGGAATGGACCATCGC  
 61 TyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrp  
 61 TACCAAGCCACCGTGTGCCTAGGGCTCAAGCCCCTCCCCATCGTGGGACCAAGATGTGG  
 ATGGTTGGTGGCACACCGATCCCGAGTCGGGGAGGGGTAGCACCCTGGTCTACACC  
 121 LysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeu  
 121 AAGTGGTTCAGAATGAAATCACCTGACGCACCCAGTCACCAAATACATCATGACATGC  
 TTCACAAACTAACGGAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGAC  
 181 GlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCys  
 181 GGCGCTTTCAGAATGAAATCACCTGACGCACCCAGTCACCAAATACATCATGACATGC  
 CCGCGACAAGTCTTACTTAGTGGACTGCGTGGTCAGTGGTTATGTAGTACTGTACG  
 241 MetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAla  
 241 ATGTCGGCCGACCTGGAGGTGTCAGCAGCACCTGGGTGCTCGTTGGCGCGTCCCTGGCT  
 TACAGCCGGCTGGACCTCCAGCAGTGCCTGTCAGGACCCACGAGCAACGCCAGGACCGA  
 301 AlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeu  
 301 GCTTGCCCGTATTGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTG  
 CGAAACCGCGCATAACGGACAGTTGTCGACGCACCAGTATCACCGTCCCAGCAGAAC  
 361 SerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMet  
 361 TCCGGGAAGCCGGCAATCATACCTGACAGGGAAAGTCCTTACCGAGAGTCGATGAGATG  
 AGGCCCTCGGCCGTTAGTATGGACTGTCCTCAGGAGATGGCTCTCAAGCTACTCTAC  
 421 GluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPhe  
 421 GAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTGCCGAGCAGTTC  
 CTTCTACGAGAGTCGTGAATGGCATGTAGCTCGTCCCTACTACGAGCGGCTCGTCAAG  
 481 LysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaPro  
 481 AAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATGCCCT  
 TTGCTCTCCGGAGCCGGAGGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGA  
 541 AlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPhe  
 541 GCTGTCCAGACCAACTGGAAAAACTCGAGACCTCTGGCGAAGCATAATGTGGAACTTC  
 CGACAGGTCTGGTTGACCGTTTTGAGCTCTGGAAGACCCGCTCGTATACACCTGAAG  
 601 IleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAla  
 601 ATCAGTGGGATACAATACTGGCGGGCTTGTCAACGCTGCCTGGTAACCCGCCATTGCT  
 TAGTCACCCTATGTTATGAACCGCCGAACAGTTGCGACGGACCATTGGGCGGTAACGA  
 661 SerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
 661 TCATTGATGGCTTTACAGCTGCTGTCACCAGCCCACAAACCACTAGCCAAA  
 AGTAACCTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTT

5/63

**FIG. 7** Translation of DNA 32

-----Overlap with 81-----

PheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeu  
 1 CTTTACAGCTGCTGTCACCAGCCCCTAAACCACTAGCCAAACCCCTCCTCTAACATAT  
 GAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTGGGAGGAAGTTGTATA

GlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAla  
 61 TGGGGGGGTGGGTGGCTGCCAGCTGCCGCCCCGGTGCCGCTACTGCCTTGTCGGCG  
 ACCCCCCCACCCACCGACGGGTCGAGCGGCCACGGCGATGACGGAAACACCCGC

GlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeu  
 121 CTGGCTTAGCTGGCGCCCATCGGCAGTGTGGACTGGGAAGGTCCCTCATAGACATCC  
 GACCGAATCGACCGCGCGGTAGCCGTACAACCTGACCCCTCAGGAGTATCTGTAGG

AlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGlu  
 181 TTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTGTGGCATTCAAGATCATGAGCGGTG  
 AACGTCCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCAC

ValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeu  
 241 AGGTCCCCTCCACGGAGGACCTGGTCAAATCTACTGCCGCATCCTCTGCCCGGAGCCC  
 TCCAGGGAGGTGCCTGGACCACTAGATGACGGCGGTAGGAGAGCGGGCCTCGGG

ValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAla  
 301 TCGTAGTCGGCGTGGTCTGTGCAGCAAACTGCGCCGGCACGTTGGCCCGGGCGAGGGGG  
 AGCATCAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCAGGGCCGCTCCCCC

ValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
 361 CAGTGCAGTGGATGAACCGGCTGATAGCCTCGCCTCCGGGGAAACCATGTTCCCC  
 GTCACTGTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTGGTACAAAGGGG

6/63

## FIG. 8 Translation of DNA 35

1 SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
 TCCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCGCACTCACGTCGGGGCAGG  
 AGGTAACCTGTAGTGCAGGGGGCCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCC

61 ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
 ACTGGCAGGGGGAAAGCCAGGCATCTACAGATTGTGGCACCGGGGAGCGCCCTCCGGC  
 TGACCGTCCCCCTCGGTCCGTAGATGTCTAACACCGTGGCCCCCTCGCGGGGAGGCCG

121 MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
 ATGTTGACTCGTCCGTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTC  
 TACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAG

181 ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
 ACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCGGGGCTCCCGTG  
 TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCAC

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241 CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
 TGCCAGGACCATCTGAATTTGGGAGGGCGTCTTACAGGCCTCACTCATATAGATGCC  
 ACGGTCCCTGGTAGAACTAAAACCTCCGCAGAAATGTCCGGAGTGAGTATATCTACGG

---

301 HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
 CACTTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAA  
 GTGAAAGATAGGGTCTGTTCGTCTCACCCCTCTGGAAAGGAATGGACCATCGCATGGTT

---

Overlap with 36

361 AlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCys  
 GCCACCGTGTGCGCTAGGGCTCAAGCCCTCCCCATCGTGGGACCAAGATGTGGAAGTGT  
 CGGTGGCACACGCGATCCCGAGTTGGGGAGGGGTAGCACCCCTGGTCTACACCTTCACA

---

421 LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla  
 TTGATTGCCTCAAGCCCACCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGCGCT  
 AACTAAGCGGAGTTGGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGA

7/63

**FIG. 9-1** Combined ORF of DNAs 35, 36, 81 & 32

1 SerIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
 TCCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCGCCTACAAACGTCGGGGCAGG  
 AGGTAACCTCTGTTAGTGCAGGGGGTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCC

61 ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
 ACTGGCAGGGGGAGCCAGGCATCTACAGATTGTGGCACCGGGGAGCGCCCTCCGGC  
 TGACCGTCCCCCTCGGTCCGTAGATGTCTAACACACCCTGGCCCCCTCGCGGGGAGGCCG

121 MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
 ATGTTCGACTCGTCCGTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTC  
 TACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAG

181 ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
 ACGCCC GCCGAGACTACAGTAGGCTACGAGCGTACATGAACACCCGGGGCTTCCCGTG  
 TGCGGGCGGCTCTGATGTCAATCCGATGCTCGCATGTACTGTGGGGCCCCGAAGGGCAC

241 CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
 TGCCAGGACCATCTGAATTGGGAGGGCGTCTTACAGGCCTCACTCATATAGATGCC  
 ACGGTCCTGGTAGAACTAAAACCCCTCCCGCAGAAATGTCCGGAGTAGTATCTACGG

301 HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
 CACTTTCTATCCCAGACAAAGCAGAGTGGGAGAACCTCCTACCTGGTAGCGTACCAA  
 GTGAAAGATAGGTCTGTTCGTCTACCCCTTGGAGGAATGGACCATCGCATGGT

361 AlaThrValCysAlaArgAlaGlnAlaProProSerTrpAspGlnMetTrpLysCys  
 GCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCATCGTGGGACCAGATGTGGAAAGTGT  
 CGGTGGCACACGCGATCCCGAGTTGGGAGGGTAGCACCCTGGTCTACACCTTCACA

421 LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla  
 TTGATTGCCCTCAAGCCCACCCCTCATGGGCCAACACCCCTGCTATACAGACTGGCGCT  
 AACTAAGCGGAGTTGGGACTGCGTGGGTACCCGGTTGTGGGACGATATGTCTGACCCGCGA

481 ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer  
 GTTCAGAATGAAATCACCCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCG  
 CAAGTCTTACTTAGGGACTGCGTGGGTCACTGGTTATGTAGTACTGTACGTACAGC

541 AlaAspLeuGluValValThrSerThrTrpValLeuValGlyValLeuAlaAlaLeu  
 GCCGACCTGGAGGTGCGTCAGGACACTGGGTGCTCGTGGCGCGCTGGCTGCTTGG  
 CGGCTGGACCTCCAGCAGTGCCTCGTGGACCCACGAGCAACGCCAGGACGACGAAAC

601 AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly  
 GCCCGTATTGCCGTCAACAGGCTGCGTGGTCAGTGGGCAGGGCGTCTGGCTCCGGG  
 CGCGCATAACGGACAGTTGTCGACGCACCAGTACCCGCTCCAGCAGAACAGGCC

661 LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu  
 AAGCCGGCAATCATACCTGACAGGGAGTCCTACCGAGAGTTGAGATGAGATGGAAGAG  
 TTCGGCCGTTAGTATGGACTGTCCTCAGGAGATGGCTCTCAAGCTACTCACCTCTC

721 CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln  
 TGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAG  
 ACGAGAGTCGTGAATGGCATGTTAGCTCGTCCCTACTACGAGCGGCTCGTCAAGTTGTC

781 LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal  
 AAGGCCCTCGGCCTCTGCAGACCGCGTCCCGTCAAGGAGGTTATGCCCTGCTGTC  
 TTCCGGGAGCCGGAGGGACGTCTGGCGAGGGCAGTCCATAGCGGGGACGACAG

841 GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer  
 CAGACCAACTGGCAAAACTCGAGACCTCTGGCGAACATATGTGGAACATTCACTCAGT  
 GTCTGGTTGACCGTTTGAGCTCTGGAAAGACCCGCTCGTATAACACCTGAAGTAGTC  
  
 901 GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu  
 GGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCGCCATTGCTTCATTG  
 CCCTATGTTATGAACCGCCCCAACAGTTGCGACGGACCATTGGGGCGGTAAACGAAGTAAC  
  
 961 MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn  
 ATGGCTTTACAGCTGCTGTCACCAGCCCACAACTAACCACTAGCCAAACCCCTCTCAAC  
 TACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGTACGGTTGGGAGGAGAAGTTG  
  
 1021 IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal  
 ATATTGGGGGGGTGGGTGGCTGCCAGCTCGCCGCCCGGTGCCGCTACTGCCTTG  
 TATAACCCCCCCCACCCACCGACGGGTCGAGCGGCCGGGCCACGGCGATGACGGAAACAC  
  
 1081 GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp  
 GGCGCTGGCTTAGCTGGCGCCCATCGGCAGTGGACTGGGAAGGTCCTCATAGAC  
 CCGCGACCGAATCGACCGCGCGGTAGCCGTACAAACCTGACCCCTCCAGGAGTATCTG  
  
 1141 IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer  
 ATCCTTGCAGGGTATGGCGCGGGCGTGGCGGGAGCTCTGTGGCATTCAAGATCATGAGC  
 TAGGAACGTCCCATAACCGCGCCCGACCGCCCTCGAGAACACCGTAAGTCTAGTACTCG  
  
 1201 GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly  
 GGTGAGGTCCCCCTCCACGGAGGACCTGGTCAATCTACTGCCGCCATCCTCTGCCCGGA  
 CCACTCCAGGGAGGTGCCTCTGGACCAGTTAGATGACGGCGGTAGGAGAGCGGGCCT  
  
 1261 AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu  
 GCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAG  
 CGGGAGCATCGCCGCACAGACACGTGTTATGACGGCGCCGTGCAACCGGGCCCGCTC  
  
 1321 GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
 GGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCGGGGAAACCATGTTCCCC  
 CCCCGTCACGTACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTGGTACAAAGGGG

FIG. 9-2

9 / 63

**FIG. 10**

## Translation of DNA 37b

1 LeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAsp  
 CTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGAC  
 GAGCGCGTTTCGACCAGCGTAACCCGTAGTTACGGCACCGGATGATGGCGCCAGAACGT

61 ValSerValIleProThrSerGlyAspValValValAlaThrAspAlaLeuMetThr  
 GTGTCCGTCATCCCGACCAGCGCGATGTTGTCGTGGCAACCGATGCCCTCATGACC  
 CACAGGCAGTAGGGCTGGTCGCCGTACAACAGCAGCACCGTTGGCTACGGGAGTACTGG

121 GlyTyrThrGlyAspPheAspSerValIleAspTyrAsnThrCysValThrGlnThrVal  
 GGCTATAACCGCGACTTCGACTCGGTGATAGACTACAATACGTGTCACCCAGACAGTC  
 CCGATATGCCGCTGAAGCTGAGCCACTATCTGATGTTATGCACACAGTGGGTCTGTCAG

-----Overlap with-----  
 181 AspPheSerLeuAspProThrPheThrIleGluThrIleLeuProGlnAspAlaVal  
 GATTTCAGCCTTGACCCCTACCTCACCATTGAGACAATACGCTCCCCCAGGATGCTGTC  
 CTAAAGTCGGAACTGGATGGAAGTGGTAACTCTGTTAGTGCAGGGGGTCTACGACAG

clone 35-----  
 SerArgThrGlnArgArgGlyArgThr  
 241 TCCCGCACTCAACGTGGGGCAGGACTG  
 AGGGCGTGAGTTGCAGCCCCGTCCTGAC

**FIG. 11**

## Translation of DNA 33b

-----Overlap with 32-----  
 MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal  
 1 GATGAACCGGCTGATAGCCTCGCCTCCGGGGAACCATGTTCCCCCACGCACTACGT  
 CTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTGGTACAAAGGGGTGCGTGTGCA

61 ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln  
 GCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCA  
 CGGCCTCTCGCTACGTCGACGGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGT

121 LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer  
 GCTCCTGAGGCAGTCGACCAAGTGGATAAGCTGGAGTGTACCACTCCATGCTCCGGTTC  
 CGAGGACTCCGCTGACGTGGTCACCTATTGAGCCTCACATGGTGAGGTACGAGGCCAAG

181 TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu  
 CTGGCTAACGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAACGACTGGCT  
 GACCGATTCCCTGTAGACCCCTGACCTATAACGCTCCACAACTCGCTGAAATTCTGGACCGA

241 LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr  
 AAAAGCTAACGCTCATGCCACAGCTGCTGGGATCCCCTTGTGTCCTGCCAGCGCGGGTA  
 TTTTCGATTGAGTACGGTGTGACGGACCCTAGGGGAAACACAGGGACGGTCCGCCCAT

301 LysGlyValTrpArgVal  
 TAAGGGGGTCTGGCGAGTG  
 ATTCCCCCAGACCGCTCAC

10/63

**FIG. 12** Translation of DNA 40b

1 AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle  
 1 GGTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCAGGGTGAGAACAAAT  
 CCGAATGTACAGGTTCCGAGTACCCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTGTTA

61 ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
 61 TACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCCTGCCGACGGCGGGTG  
 ATGGTGACCGTGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCCAC

121 SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer  
 121 CTCGGGGGCGCTATGACATAATAATTGTGACGAGTGCCACTCCACGGATGCCACATC  
 GAGCCCCCGCGAATACTGTATTATAACACTGCTCACGGTGAGGTGCCTACGGTGTAG

181 IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
 181 CATCTTGGGCATCGGCAGTCCTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGT  
 GTAGAACCGTAGCCGTGACAGGAACGGTTCTGTACGCCCCGCTCTGACCAACA

241 LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal  
 241 GCTCGCCACCGCCACCCCTCCGGCTCCGTACTGTGCCCATCCAAACATCGAGGAGGT  
 CGAGCGGTGGCGGTGGGAGGCCGAGGCACTGACACGGGGTAGGGTTGTAGCTCCTCCA

301 AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle  
 301 TGCTCTGCCACCACCGGAGAGATCCCTTTACGGCAAGGCTATCCCCCTCGAAGTAAT  
 ACGAGACAGGTGGTGGCCTCTAGGGAAAAATGCCGTTCCGATAGGGGAGCTTCATTA

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361 LysGlyGlyArgHisLeuIlePheCysHisSerLysLysCysAspGluLeuAlaAla  
 361 CAAGGGGGGGAGACATCTCATCTCTGTCAATCAAAGAAGAAGTGCAGCAACTCGCCGC  
 GTTCCCCCCCCTGTAGAGTAGAACAGTAAGTTCTTCAGCTGCTGAGCGGGCG

-----Overlap with 37b-----

421 LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
 421 AAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTGACGTGTCCGT  
 TTTCGACCAGCGTAACCGTAGTTACGGCACCGGATGATGGCGCCAGAACACTGCACAGGCA

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481 IleProThr  
 481 CATCCCGACCAAG  
 GTAGGGCTGGTC

11/63

**FIG. 13** Translation of DNA 25c

CysSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCys  
 1 ACTGCAGCCTCACTGTAACCCAGCTCCTGAGGGACTGCCACCAGTGGATAAGCTCGGAGT  
 TGACGTGGAGTGACATTGGGTCGAGGACTCCGCTGACGTGGCACCTATCGAGCCTCA

---

ThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeu  
 61 GTACCACTCCATGCTCCGGTTCTGGCTAACGGGACATCTGGACTGGATATGCGAGGTGT  
 CATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACA

---

-----Overlap with 33b-----  
 SerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPhe  
 121 TGAGCGACTTTAACACCTGGCTAAAGCTAACAGCTCATGCCACAGCTGCCTGGATCCCCT  
 ACTCGCTGAAATTCTGGACCGATTTCGAGTACGGTGTGACGGACCCCTAGGGGA

---

ValSerCysGlnArgGlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArg  
 181 TTGTGTCCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTC  
 AACACAGGACGGTCCGCCCCATATTCCCCCAGACCGCTCCCTGCCGTAGTACGTGTGAG

---

CysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGly  
 241 GCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAACGGGACGATGAGGATCGTCG  
 CGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTGCCTGCTACTCCTAGCAGC

---

ProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGly  
 301 GTCCTAGGACCTGCAGGAACATGTGGAGTGGACCTTCCCCATTAAATGCCTACACCACGG  
 CAGGATCCTGGACGTCCCTGTACACCTCACCCCTGGAAGGGTAATTACGGATGTGGTGCC

---

ProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGlu  
 361 GCCCCTGTACCCCCCTTCCCTGCGCCGAACATACGTTCGCGCTATGGAGGGTGTCTGCAG  
 CGGGGACATGGGGGGAAAGGACGGCGCTGTATGTGCAAGCGCATAACCTCCCACAGACGTC

---

GluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAsp  
 421 AGGAATATGTGGAGATAAGGCAGGTGGGGACTCCACTACGTGACGGGTATGACTACTG  
 TCCTTATACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCATACTGATGAC

---

AsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu  
 481 ACAATCTCAAATGCCGTGCCAGGTCCCATCGCCGAATTTCACAGAAT  
 TGTTAGAGTTACGGGCACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTA

12/63

**FIG. 14-1** Combined ORF of DNAs 40b/37b/35/36/81/32/33b/25c

1 AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle  
 1 TGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACC GGTTGAGAACAAAT  
 ACGAATGTACAGGTTCCGAGTACCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTAA  
  
 61 ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
 61 TACCACTGGCAGCCCCATACGTACTCCACCTACGGCAAGTTCCCTGGCCACGGCGGGTG  
 ATGGTGACCGTGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCAC  
  
 121 SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer  
 121 CTCGGGGGGCGCTTATGACATAATAATTGTGACGAGTGCCACTCCACGGATGCCACATC  
 GAGCCCCCGCGAATACTGTATTATAACACTGTCACGGTGAGGTGCCTACGGTAG  
  
 181 IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
 181 CATCTTGGGCATCGGCACTGTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGT  
 GTAGAACCGTAGCCGTGACAGGAACCTGGTCTCTGACGCCCGCTTGACCAACA  
  
 241 LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal  
 241 GCTCGCCACCGCCACCCCTCCGGGCTCCGTACTGTGCCCCATCCAACATCGAGGAGGT  
 CGAGCGGTGGCGGTGGGAGGCCGAGGCGAGTGACACGGGGTAGGGTTGTAGCTCCTCCA  
  
 301 AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle  
 301 TGCTCTGTCCACCACCGGAGAGATCCCTTTACGGCAAGGCTATCCCCCTCGAAGTAAT  
 ACGAGACAGGTGGTGGCCTCTAGGGAAAAATGCCGATAGGGGAGCTTCATTA  
  
 361 LysGlyGlyArgHisLeuIlePheCysHisSerLysLysCysAspGluLeuAlaAla  
 361 CAAGGGGGGGAGACATCTCATCTCTGTCAAAAGAAGAAGTGCACGAACTCGCCGC  
 GTTCCCCCCCCTGTAGAGTAGAACAGTAAGTTCTTCACGCTGCTGAGCGCG  
  
 421 LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
 421 AAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTGACGTGTCCTG  
 TTTCGACCAGCGTAACCGTAGTTACGGCACCGGATGATGGCGCCAGAACATGCACAGGCA  
  
 481 IleProThrSerGlyAspValValValAlaThrAspAlaLeuMetThrGlyTyrThr  
 481 CATCCGACCAGCGCGATGTTGTCGTGGCAACCGATGCCCTCATGACCGCTATAC  
 GTAGGGCTGGTCGCCGCTACAACAGCAGCACCGTTGGCTACGGAGTACTGCCGATATG  
  
 541 GlyAspPheAspSerValIleAspTyrAsnThrCysValThrGlnThrValAspPheSer  
 541 CGCGCACTTCGACTCGGTGATAGACTACAATACGTGTGTCACCCAGACAGTCGATTTCAG  
 GCCGCTGAAGCTGAGCCACTATCTGATGTTATGCACACAGTGGTCTGTCAGCTAAAGTC  
  
 601 LeuAspProThrPheThrIleGluThrIleLeuProGlnAspAlaValSerArgThr  
 601 CCTTGACCCCTACCTTACCAATTGAGACAATCACGCTCCCCCAGGATGCTGCTCCGCAC  
 GGAACGGGATGGAAGTGGTAACTCTGTTAGTGCAGGGGGTCTACGACAGAGGGCGTG  
  
 661 GlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGly  
 661 TCAACGTCGGGGCAGGACTGGCAGGGGAAGGCCAGGCATCTACAGATTGTGGCACCGGG  
 AGTTGCAGCCCCGTCCTGACCGTCCCCCTCGGTCCGTAGATGCTAAACACCGTGGCCC  
  
 721 GluArgProSerGlyMetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCys  
 721 GGAGCGCCCCCTCCGGCATGTTGCACTCGTCGTCTGTGAGTGTATGACGCAGGCTG  
 CCTCGCGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGAC  
  
 781 AlaTrpTyrGluLeuThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThr  
 781 TGCTTGGTATGAGCTACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACAC  
 ACGAACCATACTCGAGTGGGGGGCTCTGATGTCATCCGATGCTCGCATGTACTTGTG  
  
 841 ProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeu  
 841 CCCGGGGCTCCCGTGTGCCAGGACCATCTGAATTGGGAGGGCGTCTTACAGGCCT  
 GGGCCCCGAAGGGCACACGGTCTGGTAGAACTTAAACCCCTCCCGCAGAAATGTCGGGA  
  
 901 ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyr  
 901 CACTCATATAGATGCCACTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTCCTTA  
 GTGAGTATATCTACGGGTGAAAGATAAGGGTCTGTTGTCACCCCTTGGAAAGGAAT

961 LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProProSerTrpAsp  
 CCTGGTAGCGTACCAAGCCACCGTGTGCGCTAGGGCTCAAGCCCCTCCCCATCGTGGGA  
 GGACCATCGCATGGTCGGTGGCACACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCT  
 1021 GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu  
 CCAGATGTGGAAGTGTTCATTGCCTCAAGCCCACCCATGGGCCAACACCCCTGCT  
 GGTCTACACCTTCACAAACTAACGGAGTTGGACTGCGTGGTCAGTGGTTATGTA  
 1081 TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle  
 ATACAGACTGGCGCTGTTCAGAATGAAATCACCTGACGCACCCAGTCACCAAATACAT  
 TATGTCTGACCCGCGACAAGTCTTACGGACTGCGTGGTCAGTGGTTATGTA  
 1141 MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly  
 CATGACATGCATGTCGGCCGACCTGGAGGTCGTACGAGCACCTGGGTGCTCGTGGCG  
 GTACTGTACGTACAGCCGGCTGGACCTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCC  
 1201 ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg  
 CGTCCTGGCTGCTTGGCCCGTATTGCCTGTCACAGGGCTGCGTGGTCAGTGGCAG  
 GCAGGACCGACGAAACCGGCGATAACGGACAGTTGTCCGACGCACCAGTATCACCGTC  
 1261 ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe  
 GGTGCTCTGTCGGGAAGCCCGAATCATACCTGACAGGGAAAGTCCTCTACCGAGAGTT  
 CCAGCAGAACAGGCCCTCGGCCGTTAGTATGGACTGTCCCTCAGGAGATGGCTCTCAA  
 1321 AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla  
 CGATGAGATGGAAGAGTGTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCG  
 GCTACTCTACCTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTCCCTACTACGAGCG  
 1381 GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal  
 CGAGCAGTCAAGCAGAAGGCCCTCGGCCCTGCAGACCGCGTCCCGTCAGGAGAGGT  
 GCTCGTCAAGTTCGTCTCCGGGAGCCGGAGGTCTGGCGCAGGGCAGTCCGCTCCA  
 1441 IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet  
 TATCGCCCTGCTGTCAGACCAACTGGCAAAACTCGAGACCTCTGGCGAAGCATAT  
 ATAGCGGGACGACAGGTCTGGTTGACCGTTTGAGCTCTGGAAGACCCGCTCGTATA  
 1501 TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro  
 GTGGAACCTTCATCAGGGATACAATACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCC  
 CACCTTGAAGTAGTCACCCTATGTTATGAACCGCCGAACAGTTGCGACGGACCATTGGG  
 1561 AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
 CGCCATTGCTTCATTGATGGCTTTACAGCTGCTGTCACCAGCCCACAACTAGCCA  
 GCGGTAACGAAGTAACCTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTATCGGT  
 1621 ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla  
 AACCTCCTCTTCAACATATTGGGGGGGGTGGCTGCCAGCTGCCGCCCGGTGC  
 TTGGGAGGAGAAGTTGTATAACCCCCCCCACCCACCGACGGTCGAGCGGGCGGGGCCACG  
 1681 AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly  
 CGCTACTGCCTTGTGGCGCTGGCTAGCTGGCGCCCATGGCAGTGTGGACTGGG  
 GCGATGACGAAACACCCCGCACCGAACGACCGCGGGTAGCCGTACAACCTGACCC  
 1741 LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla  
 GAAGGTCTCATAGACATCCTTGAGGGTATGGCGGGCGTGGCGGGAGCTCTGTGGC  
 CTTCCAGGAGTATCTGTAGGAACGTCCCATAACGGCGCCGCACCGCCCTCGAGAACACCG  
 1801 PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla  
 ATTCAAGATCATGAGCGGTGAGGTCCCCCTCACGGAGGACCTGGTCAATCTACTGCCCGC  
 TAAGTTCTAGTACTGCCACTCCAGGGAGGTGCCTGGACCAAGTTAGATGACGGGCG  
 1861 IleLeuSerProGlyAlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHis  
 CATCCTCTGCCCGAGCCCTCGTAGTCGGCGTGGCTGTGCAGCAATACTGCCCG  
 GTAGGAGAGCGGGCCTCGGGAGCATCAGCCGCACCAAGACACGTCGTTATGACGCCCGT

FIG. 14-2 ValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArg

14/63

1921 CGTTGGCCCGGGCGAGGGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCG  
 GCAACCAGGGCCGCTCCCCGTACGTACCTACTTGGCCACTATCGGAAGCGGAGGGC  
 GlyAsnHisValSerProThrHisTyrValProGluSerAspAlaAlaAlaArgValThr  
 1981 GGGGAACCATGTTCCCCCACGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGTCAC  
 CCCCTTGGTACAAAGGGGGTGGGTATGCACGGCCTCTCGTACGTCGACGGGCGCAGTG  
 AlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSer  
 2041 TGCCATACTCAGCAGCCTCACTGTAAACCCAGCTCCTGAGGCGACTGCACCACTGGATAAG  
 ACGGTATGAGTCGTCGGAGTGACATTGGGTGAGGACTCCGCTGACGTGGTCACCTATT  
 SerGluCysThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCys  
 2101 CTCGGAGTGTACCACTCCATGCTCCGGTCTGGCTAAGGGACATCTGGACTGGATATG  
 GAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCCTGACCTATAC  
 GluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGly  
 2161 CGAGGTGTTGAGCGACTTTAACGACCTGGCTAAAGCTAAGCTCATGCCACAGCTGCCTGG  
 GCTCCACAACTCGCTGAAATTCTGGACCGATTTCGAGTACGGTGTGACGGACC  
 IleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMet  
 2221 GATCCCCTTGTGTCCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCAT  
 CTAGGGGAAACACAGGACGGTGCAGCCCATATTCCCCAGACCGCTCACCTGCCGTAGTA  
 HisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArg  
 2281 GCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAAACGGGACGATGAG  
 CGTGTGAGCGACGGTGACACCTCGACTCTAGTGACCTGTACAGTTTGCCCTGCTACTC  
 IleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyr  
 2341 GATCGTCGGCCTAGGACCTGCAGGAACATGTGGAGTGGACCTTCCCCATTAATGCCTA  
 CTAGCAGCCAGGATCCTGGACGTCCTGTACACCTCACCTGGAAAGGGTAATTACGGAT  
 ThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgVal  
 2401 CACCACGGGCCCCCTGTACCCCCCTTCCCTGCCCGAACTACACGTTCGCCTATGGAGGGT  
 GTGGTGCCCCGGGACATGGGGGAAGGACGCGGTTGATGTGCAAGCGCATACTCCCA  
 SerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMet  
 2461 GTCTGCAGAGGAATATGTGGAGATAAGGCAGGTGGGGACTTCCACTACGTGACGGGTAT  
 CAGACGTCTCCTTATACACCTCTATTCCGTCCACCCCTGAAGGTGATGCACTGCCATA  
 ThrThrAspAsnLeuLysCysProCysGlnValProSerProGluPhePheThrGlu  
 2521 GACTACTGACAATCTCAAATGCCGTGCCAGGTCCATGCCCGAATTTTCACAGAAAT  
 CTGATGACTGTTAGAGTTACGGCACGGTCCAGGGTAGCGGGCTAAAAAGTGTCTTA

FIG. 14-3

## FIG. 15 Translation of DNA 33c

1 AlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPheThr  
 1 GCGGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAAACCATGAGGTCCCCGGTGTTCAC  
 CCGCCACCTGAAATAGGGACACCTCTTGGATCTGTGGTACTCCAGGGGCCACAAGTG  
 61 AspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAlaPro  
 61 GGATAACTCCCTCACCAGTAGTGCCTCAGAGCTTCCAGGTGGCTCACCTCATGCTCC  
 CCTATTGAGGAGAGGGTGGTCATCACGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGG  
 121 ThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysVal  
 121 CACAGGCAGCGGCAAAAGCACCAAGGTCCCCTGCATATGCAGCTCAGGGCTATAAGGT  
 GTGTCCCGTCCGGTTTCGTGGTCCAGGGCCGACGTACGTCGAGTCCCCTATTCCA  
 181 LeuValLeuAsnProSerValAlaAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAla  
 181 GCTAGTACTCAACCCCTCTGTTGCTGCAACACTGGCTTGGCTTACATGTCCTAACGGC  
 CGATCATGAGTTGGGAGACAACGACGTTGACCCGAAACCACGAATGTACAGGTTCCG  


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 241 Overlap with 40b—  
 HisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIle  
 241 TCATGGGATCGATCTAACATCAGGACCGGGTGAGAACAAATTACCAACTGGCAGCCCCAT  
 AGTACCCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTGTTAATGGTGACCGTCGGGTA  
 301 ThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAsp  
 301 CACGTACTCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGCGCTTATGA  
 GTGCATGAGGTGGATGCEGTTCAAGGAACGGCTGCCACGAGCCCCCGCGAATACT  
 361 IleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThr  
 361 CATAATAATTGACGAGTGCCACTCCACGGATGCCACATCCATCTGGGATTGGCAC  
 GTATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTAGGTAGGAACCCGTAACCGTG  
 421 ValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrPro  
 421 TGTCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACGCCACCC  
 ACAGGAACGGTTCGTCTGACGCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGG  
 481 ProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGly  
 481 TCCGGGCTCCGTACTGTGCCCCATCCAAACATCGAGGAGGTGCTCTGTCCACCACCG  
 AGGCCCGAGGCAGTGACACGGGTAGGGTTAGCTCCTCCAACGAGACAGGTGGTGGC  
 541 GluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeu  
 541 AGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCT  
 TCTCTAGGGAAAAATGCCGTCCTCGATAGGGGAGCTTCATTAGTCCCCCTCTGTAGA  
 601 IlePheCysHisSerLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGly  
 601 CATCTTCTGTCATTCAAAGAAGAAGTGCACGAACTCGCCGCAAAGCTGGTCGCATTGGG  
 GTAGAACAGTAAGTTCTTACGCTGCTTGAGCGCGTTCGACCAGCGTAACCC  
 661 IleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAsp  
 661 CATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTATCCCGACCAGCGGGGA  
 GTAGTTACGGCACCCGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCT  
 721 ValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerVal  
 721 TGTGTCGTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCACTTCGACTCGGT  
 ACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCGATATGGCCCTGAAGCTGAGCCA  
 781 IleAspCysAsnThrCys  
 781 GATAGACTGCAATACTGTG  
 CTATCTGACGTTATGCACAC

16 / 63

**FIG. 16 Translation of DNA 8h**

ProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIlePro  
 1 CTCCTGCACCTGGGCTCTCGGACCTTACCTGGTCACGAGGCACGCCATGTCATT  
 GAGGGACGTGAACGCCAGGAGCTGGAAATGGACCAGTGCTCCGTGCGGCTACAGTAAG

ValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeu  
 61 CCGTGCACGGCGGGGGTGTAGCAGGGGCAGCCTGCTGCCCCGGCCATTCTACT  
 GGCACGCCGCCCCACTATCGTCCCCGTCGGACAGCGGGGCCGGTAAAGGATGA

LysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArg  
 121 TGAAAGGCTCCTCGGGGGTCCGCTGTTGCCCCGCGGGCACGCCGTGGCATATTAA  
 ACTTTCCGAGGAGCCCCCAGGCGAACACACGGGGCGCCCCGTGCGGCACCGTATAAAAT

---

Overlap with

AlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIleProValGluAsnLeu  
 181 GGGCGCGGTGTGCACCCGTGGAGTGGCTAAGGCGGTGGACTTTATCCCTGTGGAGAAC  
 CCCGGGCCACACGTGGCACCTCACCAGTGGCATCGAACTGAAATAGGGACACCTCTTGG

33c

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GluThrThrMetArgSerProValPheThrAspAsnSer  
 241 TAGAGACAACCATGAGGTCCCCGGTGTACGGATAACTCCTC  
 ATCTCTGTTGGTACTCCAGGGGCCACAAGTGCCTATTGAGGAG

**FIG. 17 Translation of DNA 7e**

GlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGly  
 1 GGGGTGGAGGTTGCTGGGCCATCACGGCGTACGCCAGCAGACAAGGGCCTCTAGG  
 CCCCACCTCCAACGACCGCGGGTAGTGCCGCATGCGGGTGTCTGTTCCCGGAGGATCC

CysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIle  
 61 GTGCATAATCACCAGCCTAACTGGCCGGACAAAACAAGTGGAGGGTAGGTCCAGAT  
 CACGTATTAGTGGTCGGATTGACCGGCCCTGTTTGGTACCTCCCACCTCCAGGTCTA

ValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrVal  
 121 TGTGTCAACTGCTGCCAACCTCTGGCAACGTGCATCAATGGGTGTGCTGGACTGT  
 ACACAGTTGACGACGGTTGGAAGGACCGTTGACGTAGTTACCCCACACGACCTGACA

TyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyr  
 181 CTACCACGGGGCCGGAACGAGGACCATCGCGTCACCAAGGGCTGTACAGATGTA  
 GATGGTGCCCCGGCCTTGCTCCTGGTAGCGCAGTGGTTCCCAGGACAGTAGGTCTACAT

ThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThr  
 241 TACCAATGTAGACCAAGACCTTGTGGGCTGGCCCGCTCGCAAGGTAGCCGCTATTGAC  
 ATGGTTACATCTGGTTCTGGAACACCCGACCGGGCGAGGCGTTCCATCGCGAGTAACATG

---

Overlap with 8h

ProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHis  
 301 ACCCTGCACCTGGGCTCTCGGACCTTACCTGGTCACGAGGCACG  
 TGGGACGTGAACGCCAGGAGCCTGGAAATGGACCAGTGCTCCGTGC

17/63

## FIG. 18 Translation of DNA 14c

AsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeu  
 1 GAAACATGTGGAGTGGGACCTCCCCATTAAATGCCCTACACCACGGGCCCCTGTACCCCCCT  
 CTTGTACACCTCACCCCTGGAAAGGGTAATTACGGATGTGGTGCCCCGGGACATGGGGGA

---

Overlap with 25c

ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle  
 61 TCCCTGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGAT  
 AGGACGCGGCCCTGATGTGCAAGCGCGATACTCCCCACAGACGTCTCCTATGCACCTCTA

---

ArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro  
 121 AAGGCAGGTGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTAAATGCC  
 TTCCGTCCACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTACGGG

---

CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe  
 181 GTGCCAGGTCCCCTCGCCCGAATTTCACAGAATTGGACGGGGTGCCTACATAGGTT  
 CACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTAACCTGCCACCGCGATGTATCAA

AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu  
 241 TGCGCCCTCTGCAAGCCCTGCTGCGGGAGGGAGGTATCATTGAGTAGGACTCCACGA  
 ACCGGGGGGACGTCGGAAACGACGCCCTCCATAGTAAGTCTCATCCTGAGGTGCT

TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer  
 301 ATACCCGGTAGGGTCGCAATTACCTTGGAGCCCGAACCGGAGTGGCGTGTGACGTC  
 TATGGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCAACGGCACACTGCAG

MetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGly  
 361 CATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGAAAGGTTGGCGAGGGGG  
 GTACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCTCCAACCGCTCCCC

SerProProSerValAlaSerSerAlaSerGlnLeuSerAlaProSerLeuLysAla  
 421 ATCACCCCTCTGTTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGC  
 TAGTGGGGGGAGACACCGGTGAGGAGCCGATCGGTGATAGGGAGGTAGAGAGTTCCG

ThrCysThrAlaAsnHisAspSerProAsp  
 481 AACTTGCACCGCTAACCATGACTCCCCCTGAT  
 TTGAACGTGGCGATTGGTACTGAGGGGACTA

19/63

## FIG. 19 Translation of DNA 8f

Overlap with 14c

1 SerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThrAlaAsnHis  
 AGCTCCTCGGCTAGGCCAGCTATCCGCTCCATCTCAAGGCAACTTGCACCGCTAACCAT  
 TCGAGGAGCCGATCGGTGATAGGCAGGGTAGAGAGTTCCGTTGAACGTGGCGATTGGTA

61 AspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGly  
 GACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGGCGGC  
 CTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTCTACCCSCCG

121 AsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSerPheAspProLeu  
 AACATCACCAAGGGTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCCTCGATCCGCTT  
 TTGTAGTGGTCCCAACTCAGTCCTTGTTCACCACTAACGACTGAGGAAGCTAGGCAGAA

181 ValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArgLysSerArg  
 GTGGCGGAGGAGGACGAGCAGGGAGATCTCCGTACCCGAGAAATCCTGCGGAAGTCTCGG  
 CACCGCCTCCTCGCTCGCCCTCTAGAGGCATGGCGTCTTAGGACGCCCTCAGAGCC

241 ArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProProLeuValGlu  
 AGATTGCCCCAGGCCCTGCCGTTGGCGCGCCGGACTATAACCCCCCGCTAGTGGAG  
 TCTAACGGGTCCGGGACGGGAAACCCGCGCCGCTGATATTGGGGGGCGATCACCTC

301 ThrTrpLysLysProAspTyrGluProProValValHisGlyCysProLeuProProPro  
 ACGTGGAAAAAGCCCACTACGAACCACCTGTGGTCCATGGCTGCGCTTCCACCTCCA  
 TGACACCTTTTCGGGCTGATGCTGGTGGACACCAGGTACCGACAGGCGAAGGTGGAGGT

361 LysSerProProValPro  
 AAGTCCCCCTCGTGC  
 TTCAGGGAGGACACGGC

## FIG. 20 Translation of DNA 33f

Overlap with 8f

1 ValTrpAlaArgProAspTyrAsnProProLeuValGluThrTrpLysLysProAspTyr  
 CGTTGGCGCGGCCGGACTATAACCCCCCGTAGTGGAGACGTGGAAAAAACCGACTA  
 GCAAACCCGCGCCGGCCTGATATTGGGGGGCGATCACCTCTGCACCTTTTGGGCTGAT

61 GluProProValValHisGlyCysProLeuProProProLysSerProProValProPro  
 CGAACCACCTGTGGTCCATGGCTGCCGCTTCCACCTCCAAAGTCCCTCTGTGCCTCC  
 GCTTGGTGGACACCAGGTACCGACGGCGAAGGTGGAGGTTCAAGGGAGGACACGGAGG

121 ProArgLysLysArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAlaGlu  
 GCCTCGGAAGAACGGGACGGTGGTCCACTGAATCACCCCTACTACTGCGCTTGGCCGA  
 CGGAGCCTCTCGCCTGCCACCAGGAGTGACTTAGTGGGATAGATGACCGAACCCGGCT

181 LeuAlaThrArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThr  
 GCTCGCCACCAGAACGCTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATACGAC  
 CGAGCGGTGGTCTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTATGCTG

241 ThrSerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerPhe  
 AACATCCCTGAGGCCGCCCTCTGGCTGCCCGGGACTCCGACGCTGAGTCCCTTGC  
 TTGTAGGAGACTCGGGCGGGGAAGACCGACGGGGGGCTGAGGCTGCGACTCAGGAAACG

19/63

## FIG. 21 Translation of DNA 33g

1 AlaSerArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThrThr  
 GCCTCCAGAAGCTTGGCAGCTCCTCAACTCCGGCATTACGGGCGACAATACGACAACA  
 CGGAGGTCTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTATGCTGTGT

---

Overlap with 33f

61 SerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSer  
 TCCTCTGAGCCCCGCCTCTGGCTGCCCGACTCCGACGCTGAGTCCTATTCCCTCC  
 AGGAGACTCGGGCGGGAAAGACCGACGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGG

121 MetProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThr  
 ATGCCCCCCCCTGGAGGGGGAGCCTGGGATCCGGATCTTAGCGACGGGTATGGTCAACG  
 TACGGGGGGGACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCAGTACCAAGTIGC

181 ValSerSerGluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThr  
 GTCACTAGTGAGGCCAACGCGGAGGATGTCGTGCTGCTCAATGCTTACTCTGGACA  
 CAGTCATCACTCCGGTTGCCCTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGT

241 GlyAlaLeuValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSer  
 GGCGCACTCGTCACCCCGTGGCGCCGCGGAAGAACAGAAACTGCCATCAATGCACTAACG  
 CGCGTGAGCAGTGGGGCACCGGGCCCTCTGCTTIGACGGTAGTTACGTGATTG

301 AsnSerLeuLeuArgHisHisAsnLeuValTyrSerThrThrSerArgSer  
 AACTCGGTCTACGTCACCACAATTGGTAGAGTGAGGAGAACCCCTGACCGCGTGTGCCGAACG  
 TTGAGCAACGATGCACTGGTTAAACCACATAAGGTGGAGTGCAC

## FIG. 22 Translation of DNA 7f

1 GlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArg  
 GGCACCTATGTTATAACCATCTCACTCCTCTCGGGACTGGGCGACAACGGCTTGC  
 CGTGGATACAAATATTGGTAGAGTGAGGAGAACCCCTGACCGCGTGTGCCGAACGCT

61 AspLeuAlaValAlaValGluProValValPheSerGlnMetGluThrLysLeuIleThr  
 GATCTGGCCGTGGCTGTAGAGCCAGTCGTCTCTCCCAAATGGAGACCAAGCTCATCACG  
 CTAGACCGGCACCGACATCTCGGTACGCAGAACAGAGGGTTACCTCTGGTTCGAGTAGTC

121 TrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArg  
 TGGGGGGCAGATAACGCCGCGTGCCTGACATCATCAACGGCTGCCTGTTCCGCC  
 ACCCCCCGTCTATGGCGGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGGCGGGCG

---

181 ArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeu  
 AGGGGGCCGGGAGATACTGCTCGGGCCAGCCGATGGAATGGTCTCCAAGGGTTGGAGGGTG  
 TCCCCGGCCCTCTATGACGAGCCGGCTACCTTACCAAGAGGTTCCCAACCTCCAAC

---

241 LeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThr  
 CTGGCGCCCATCACGGCGTACGCCAGCAGACAAGGGGCTCTAGGGTGCATAATCAC  
 GACCGCGGGTAGTGCCGCATGCCGCTGTTCCCCGGAGGATCCCACGTATTAGTGG

---

Overlap with 7e

301 SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla  
 AGCCTAACTGGCCGGGACAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCACGT  
 TCGGATTGACCGGCCCTGTTGGTTCACCTCCACTCCAGGTCTAACACAGTTGACGA

---

361 AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrp  
 GCCCAAACCTTCCGGCAACGTGCATCAATGGGGTGTGCTGG  
 CGGGTTGGAAAGGACCGTGCACGTAGTTACCCACACGACC

20/63

**FIG. 23** Translation of DNA 11b

GlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyr  
 1 GGCGGTGTTGTTCTCGTCGGGTTGATGGCGCTGACTCTGTACCATATTACAAGCGCTAT  
 CCGCCACAACAAGAGCAGCCAACTACCGCGACTGAGACAGTGGTATAATGTCGCGATA

IleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHis  
 61 ATCAGCTGGTGTGCTTGTGGCTTCAGTATTCTGACCAGAGTGGAAAGCGCAACTGCAC  
 TAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTCGCGTTGACGTG

ValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeuMetCys  
 121 GTGTGGATTCCCCCCCCTAACGTCCGAGGGGGCGCGACGCCGTACCTACTCATGTGT  
 CACACCTAACGGGGGGAGTTGCAGGCTCCCCCGCGCTGCCGCAGTAGAATGAGTACACA

AlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPheGlyPro  
 181 GCTGTACACCCGACTCTGGTATTGACATACCAAATTGCTGCTGGCGTCTTCGGACCC  
 CGACATGTGGGCTGAGACCATAAACTGTAGTGGTTAACGACGACCGGCAGAACGCTGGG

LeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGlnGlyLeu  
 241 CTTTGGATTCTTCAAGCCAGTTGCTTAAAGTACCCCTACTTGTGCGCGTCCAAGGCCTT  
 GAAACCTAACGAGTTCGGTCAAACGAATTGATGGGATGAAACACGCGCAGGTTCCGGAA

LeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMetValIle  
 301 CTCCGGTTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATC  
 GAGGCCAACGACGCGCAATCGCGCTCTACTAGCCTCCGGTAATGCACGTTACCACTAG

---

IleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeuArgAsp  
 361 ATTAAGTTAGGGCGCTACTGGCACCTATGTTATAACCATCTCACTCCTCTCGGGAC  
 TAATTCAATCCCCCGCAATGACCGTGGATACAAATATTGGTAGAGTGAGGAGAACCGCTG

-----Overlap with 7f-----  
 TrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPheSerGln  
 421 TGGGCGCACAAACGGCTTGCAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTCTCCAA  
 ACCCGCGTGTGCCGAACGCTCTAGACCGGCACCGACATCTCGGTCAAGCAGAACGAGGGTT

-----  
 MetGluThrLysLeuIleThrTrpGly  
 481 ATGGAGACCAAGCTCATCACGTGGGGGGC  
 TACCTCTGGTTCGAGTAGTGCACCCCCCG

21/63

**FIG. 24** Translation of DNA 14i

GluTyrValValLeuLeuPheLeuLeuLeuAlaAspAlaArgValCysSerCysLeuTrp  
 1 GGGAGTACGTCGTTCTCCTGTCCCTCTGCTTGAGACGCCGCGCTGCTCCTGCTTGT  
 CCCTCATGCAGCAAGAGGAAGACGAACGTCCTGCGCGCAGACGAGGACGAACA

MetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAla  
 61 GGATGATGCTACTCATATCCCAAGCGGGAGGCGGCTTGGAGAACCTCGTAATACTTAATG  
 CCTACTACGATGAGTATAGGGTTCGCCTCCGCGAACCTCTGGAGCATTATGAATTAC

AlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrp  
 121 CAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTCCTCGTGTCTGCTTGCAT  
 GTCGTAGGGACCAGGCCCTGCGTGCAGAACATAGGAAGGAGCACAAAGAACGAAACGTA

TyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeu  
 181 GGTATTGAAAGGGTAAGTGGGTGCCCGAGCGGTCTACACCTCTACGGGATGTGGCCTC  
 CCATAAACCTCCCATTCAACCCACGGGCCTGCCAGATGTGGAAGATGCCCTACACGGAG

LeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAla  
 241 TCCTCCTGCTCCTGTGGCGTTGGCGCTGCCCGAGCGCCTGGACACGGAGGTGGCCG  
 AGGAGGACGAGGACAACCGCAACGGGTGCCGCATGCCGACCTGTGCCCTCACCGGC

-----Overlap with 11b-----  
 SerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLys  
 301 CGTCGTGGCGGTGTTGTTCTCGTGGCTGACTCTGTCACCATATTACA  
 GCAGCACACCGCCACAAGAGCAGCCAACTACCGCGACTGAGACAGTGGTATAATGT

-----  
 ArgTyrIleSerTrpCysLeuTrpTrpLeuGln  
 361 AGCGCTATATCAGCTGGTGTGTTGGCTCAGAA  
 TCGCGATATAGTCGACCACGAACACCACCGAAGTCTT

**FIG. 25** Translation of DNA 39c

ProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProPro  
 1 CCAGCCCCCTCTGGCTGCCCGACTCCGACGCTGAGTCTATTCCATGCCCG  
 GGTGGGGAAAGACCGACGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGG

LeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSer  
 61 CTGGAGGGGGAGCCTGGGATCCGGATCTTAGCGACGGGTAGGTCAACAGTCAGTAGT  
 GACCTCCCCCTCGGACCCCTAGGCCTAGAAATCGCTGCCAGTACCGAGTTGTCAGTCATCA

-----Overlap with 33g-----  
 GluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeu  
 121 GAGGCCAACCGGGAGGATGTCGTGTGCTCAATGCTACTCTTGGACAGGGCAGACTC  
 CTCCGGTTGCGCCTCCTACAGCACACGACGAGTTACAGGATGAGAACCTGTCCCGTGTGAG

ValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeu  
 181 GTCACCCCGTGCAGCGGAGAAACAGAACTGCCATCAATGCACTGAGCAACTCGTTG  
 CAGTGGGGCACGCCCTCTGTGACGGGTAGTTACGTGACTCGTTGAGCAAC

LeuArgHisHisAsnLeuValTyrSerThrSerArgSerAlaCysGlnArgGlnLys  
 241 CTACGTACCAACAAATTGGTGTATTCCACCACTCACGAGTGCTGCCAAAGGCAGAAG  
 GATGCAGTGGTGTAAACCACATAAGGGTGGAGTGCACGAAACGGTTCCGTCTTC

LysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGlu  
 301 AAAGTCACATTTGACAGACTGCAAGTTCTGGACAGCCATTACAGGACGTACTCAAGGAG  
 TTTCAGTGTAAACTGTCGACGTTCAAGACCTGTCGGTAATGGCCTGCATGAGTTCTC

ValLysAlaAlaAlaSerLysValLysAlaAsnPhe  
 361 GTTAAAGCAGCGCGTCAAAAGTGAAGGCTAACTTC  
 CAATTCGTCGCCGAGTTTCACTTCCGATTGAAG

22/63

**FIG. 26-1 COMBINED ORF OF DNAs**  
 14i/11b/7f/7e/8h/33c/40b/37b/35/36/81/32/33b/25c/14c/8f/33g/39c

1 GluTyrValValLeuLeuPheLeuLeuAlaAspAlaArgValCysSerCysLeuTrp  
 GGGAGTACGTCGTTCTCCTGTTCTGCTGCAGACGCCGCGTCTGCTCCTGCTTG  
 CCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCCGCCAGACGAGGACGAACA  
  
 61 MetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsnLeuValIleLeuAsnAla  
 GGATGATGCTACTCATATCCAAAGCGGGAGGCGGCTTGGAGAACCTCGTAATACTTAATG  
 CCTACTACGATGAGTATAGGGTCCGCCAGAACCTCTGGAGCATTATGAATTAC  
  
 121 AlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuValPhePheCysPheAlaTrp  
 CAGCATCCCTGGCCGGGACGCACGGCTTGATCACCTCTCGTCTCTGCTTGCAT  
 GTCGTAGGGACCAGGCCCTCGGTGCCAGAACATAGGAAGGAGCACAAGAACGAAACGTA  
  
 181 TyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPheTyrGlyMetTrpProLeu  
 GGTATTTGAAGGTAAGTGGGTGCCGGAGCGGTCTACACCTCTACGGGATGTGGCCTC  
 CCATAAACTCCCCATCACCCACGGGCCTCGCCAGATGTGGAAGATGCCCTACACGGAG  
  
 241 LeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeuAspThrGluValAlaAla  
 TCCTCCTGCTCCTGTTGGCGTGGCCCCAGCGGGCGTACGCCGTGGACACGGAGGTGGCCG  
 AGGAGGACGAGGACAACCGAACGGGTCGCCATGCCGACCTGCGCTCCACCGGC  
  
 301 SerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThrLeuSerProTyrTyrLys  
 CGTCGTGTGGCGGTGTTGTCGTTGACTCTGTCACCATAATTACA  
 GCAGCACACCGCCACAACAAGAGCAGCCAACCGCGACTGAGACAGTGGTATAATGT  
  
 361 ArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeuThrArgValGluAlaGln  
 AGCGCTATATCAGCTGGTGTGCTGGCTTCAGTATTTCTGACCAGAGTGGAAAGCGC  
 TCGCGATATAGTCGACCACGAACACCACCGAAGTCATAAAAGACTGGTCTCACCTCGCG  
  
 421 LeuHisValTrpIleProProLeuAsnValArgGlyGlyArgAspAlaValIleLeuLeu  
 AACTGCACGTGTGGATTCCCCCCCCTCAACGTCCGAGGGGGCGCGACGCCGTCTTAC  
 TTGACGTGCACACCTAACGGGGGGAGTTGCAGGCTCCCCCGCGCTGCCAGTAGAATG  
  
 481 MetCysAlaValHisProThrLeuValPheAspIleThrLysLeuLeuLeuAlaValPhe  
 TCATGTGTGCTGTACACCCGACTCTGGTATTTGACATACCAAATTGCTGCTGGCGTCT  
 AGTACACACGACATGTGGCTGAGACCATAACTGTAGTGGTTAACGACGACCGGCAGA  
  
 541 GlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValProTyrPheValArgValGln  
 TCGGACCCCTTGGATTCTTCAAGCCAGTTGCTAAAGTACCCCTACTTGCGCGTCT  
 AGCCTGGGAAACCTAACAGAAGTCGGTCAAACGAATTGAAACACCGCGCAGG  
  
 601 GlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGlyGlyHisTyrValGlnMet  
 AAGGCCTTCTCCGGTCTGCGCGTTAGCGCGGAAGATGATCGGAGGCCATTACGTGCAA  
 TTCCGGAAAGAGGCCAACGCGCAATCGCCCTACTAGCCTCCGGTAATGCACGTT  
  
 661 ValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyrAsnHisLeuThrProLeu  
 TGGTCATCATTAAGTTAGGGCGCTTACTGGCACCTATGTTATAACCATCTCACTCCTC  
 ACCAGTAGTAATTCAATCCCCCGCAATGACCGTGGATACAAATATTGGTAGAGTGAGGAG  
  
 721 ArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAlaValGluProValValPhe  
 TTCGGGACTGGCGCACACGGCTTGCGAGATCTGGCGTGGCTGTAGAGCCAGTCGTCT  
 AAGCCCTGACCCCGCGTGTGCCGAACGCTCTAGACCGGACCGACATCTGGTCAGCAGA  
  
 781 SerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThrAlaAlaCysGlyAspIle  
 TCTCCCCAAATGGAGACCAAGCTCATCACGTGGGGCAGATAACGCCCGTGCAGGTGACA  
 AGAGGGTTACCTCTGGTCAGTAGTGCACCCCCCGTCTATGGCGCGCACGCCACTGT  
  
 841 IleAsnGlyLeuProValSerAlaArgArgGlyArgGluIleLeuGlyProAlaAsp  
 TCATCAACGGCTTGCGCTGTTCCGCCGCAGGGGCCGGAGATACTGCTCGGGCCAGCCG  
 AGTAGTTGCCGAACGGACAAAGGCCGGCGTCCCCGGCCCTATGACGAGGCCGGTCGGC  
 GlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThrAlaTyrAlaGlnGlnThr

23/63

901 ATGGAATGGTCTCCAAGGGGTGGAGGTGCTGGCGCCCATCACGGCGTACGCCAGCAGA  
TACCTTACCAAGAGGTTCCCCACCTCCAACGACCGCGGTAGTGCCGCATGCCGGTCGTCT

961 ArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArgAspLysAsnGlnValGlu  
CAAGGGGCCTCCTAGGTGCATAATCACAGCCTAACTGCCGGACAAAAACCAAGTGG  
GTTCCCCGGAGGATCCCACGTATTAGTGGTCGGATTGACCGGCCCTGTTGGTTCAAC

1021 GlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGly  
AGGGTGAGGTCCAGATTGTGTCAGTGCCTGCCAACCTTCCTGGCAACGTGCATCAATG  
TCCCACCTCCAGGTCTAACACAGTTGACGACGGTTGGAAGGACCGTTGCACGTAGTTAC

1081 ValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyPro  
GGGTGTGCTGGACTGTCTACCACGGGGCCGGAACGAGGACCATCGCGTCACCCAAGGGTC  
CCCACACGACCTGACAGATGGTGCCTGGCTCTGGTAGCGCAGTGGTTCCAC

1141 ValIleGlnMetTyrThrAsnValAspGlnAspLeuValGlyTrpProAlaProGlnGly  
CTGTCATCCAGATGTATACCAATGTAGACCAAGACCTTGTGGCTGGCCGCTCCGCAAG  
GACAGTAGGTCTACATATGGTTACATCTGGTCTGGAACACCCGACCGGGCGAGGCGTTC

1201 SerArgSerLeuThrProCysThrCysGlySerSerAspLeuTyrLeuValThrArgHis  
GTAGCCGCTCATTGACACCCCTGCACTTGCCTCGGACCTTACCTGGTCACGAGGC  
CATCGGCGAGTAACGTGGACGTGAAACGCCGAGGAGCCTGGAAATGGACCAAGTGTCTCCG

1261 AlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLeuSerProArg  
ACGCCGATGTCATTCCCGTGCGCCGGGGGTGATAGCAGGGGCAGCCTGCTGTCGCC  
TGGCGCTACAGTAAGGGCACCGGGCCCCACTATCGTCCCCGTGGACGACAGCGGGG

1321 ProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAla  
GGCCCATTCTCCTACTTGAAAGGCTCCTCGGGGGGTCCGCTGTTGTGCCCGCGGGGCACG  
CCGGGTAAAGGATGAACTTCCGAGGAGCCCCCAGGCGACAACACGGGGCGCCCGTGC

1381 ValGlyIlePheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAspPheIle  
CCGTGGGCATATTTAGGGCCGCGGTGTCACCCGTGGAGTGGCTAAGGCGGTGGACTTTA  
GGCACCCGTATAAACCGGGCGCACACGTGGCACCTCACGATTCCGCCACCTGAAAT

1441 ProValGluAsnLeuGluThrThrMetArgSerProValPheThrAspAsnSerSerPro  
TCCCTGTGGAGAACCTAGAGACAACCATGAGGTCCCGGTGTTACGGATAACTCCTCTC  
AGGGACACCTCTGGATCTGTGGTACTCCAGGGGCCACAAGTGCCTATTGAGGAGAG

1501 ProValValProGlnSerPheGlnValAlaHisLeuHisAlaProThrGlySerGlyLys  
CACCAAGTGGCTCCAGAGCTTCCAGGTGGCTCACCTCCATGCTCCACAGGCAGCGGC  
GTGGTCATCACGGGTCTCGAAGGTCCACCGAGTGGAGGTACGAGGGTGTCCCGTCCGT

1561 SerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsnPro  
AAAGCACCAAGGTCCCGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAACC  
TTTCGTGGTCCAGGGCGACGTACGTCAGTCCGATATTCCACGATCATGAGTTGG

1621 SerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAspPro  
CCTCTGTGCTGCAACACTGGGCTTGGTCTACATGTCCAAGGCTCATGGGATCGATC  
GGAGACACGACGTGACCCGAAACACGAATGTACAGGTTCCGAGTACCCCTAGCTAG

1681 AsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThrTyr  
CTAACATCAGGACGGGGGTGAGAACAAATTACCAACTGGCAGCCCCATACGTACTCCACCT  
GATTGTAGTCCTGGCCCCACTCTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGGA

1741 GlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCysAsp  
ACGGCAAGTCCCTGCCGACGGCGGGTGCTCGGGGGCGCTTATGACATAATAATTGTC  
TGCGTTCAAGGAACGGCTGCCACGAGCCCCCGCGAATAACTGTATTATAAACAC

1801 GluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGlnAla  
ACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATGGCACTGTCCCTGACCAAG  
TGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGCCGTGACAGGAACGGTTC

1861 GluThrAlaGlyAlaArgLeuValLeuAlaThrAlaThrProProGlySerValThr  
CAGAGACTGCGGGGGCGAGACTGGTTGTGCTGCCACCGCCACCCCTCCGGGCTCCGTCA  
GTCTCTGACGCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCGAGGCAGT

FIG. 26-2.

SIRSTITIUTE SHEET

24 / 63

1921 ValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPheTyr  
 CTGTCCCCATCCAAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT  
 GACACGGGGTAGGGTTGTAGCTCTCAACGAGACAGGTGGTGGCTCTCTAGGGAAAAA  
  
 1981 GlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHisSer  
 ACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGACATCTCATCTGTCAATT  
 TGCCGTTCCGATAGGGGGAGCTTCATTAGTCCCCCTCTGTAGAGTAGAACAGTAA  
  
 2041 LysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaValAla  
 CAAAGAAGAAGTGCACGAACTCGCCGAAAGCTGGTCGATTGGGCATCAATGCCGTGG  
 GTTTCTTCTCACGCTGCTTGAGCGCGTTCGACCAGCGTAACCGTAGTTACGGCACC  
  
 2101 TyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValAla  
 CCTACTACCGCGGTCTTGACGTGTCGATCCCCGACCGCGGCGATGTTGTCGTCGTGG  
 GGATGATGGCGCCAGAACCTGCACAGGCACTAGGGCTGGTCGCCCTACAACAGCAGCACC  
  
 2161 ThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsnThr  
 CAACCGATGCCCTCATGACCGGCTATAACCGGCGACTTCGACTCGGTGATAGACTGCAATA  
 GTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTAT  
  
 2221 CysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIleThr  
 CGTGTGTCACCCAGACAGTCGATTCTGACGCTTGACCTTACCCATTGAGACAAATCA  
 GCACACAGTGGGTCTGTCAGCTAAAGTCGGAACGGATGGTAAGTGGTAACTCTGTTAGT  
  
 2281 LeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLysPro  
 CGCTCCCCCAGGATGCTGCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGAAGC  
 GCGAGGGGGTCCTACGACAGAGGGCGTGAGTGCAGCCCCGTCCTGACCGTCCCCCTCG  
  
 2341 GlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSerVal  
 CAGGCATCTACAGATTGTCGACCGCCCTCCGGCATGTTGACTCGTCCCG  
 GTCCGTAGATGCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGC  
  
 2401 LeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThrThr  
 TCCTCTGTGAGTGCCTATGACCGCAGGCTGTGCTGGTATGAGCTCACGCCCGAGACTA  
 AGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCAGGGCGCTCTGAT  
  
 2461 ValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeuGlu  
 CAGTTAGGCTACGAGCGTACATGAACACCCGGGGCTCCCGTGTGCCAGGACCATCTTG  
 GTCAATCCGATGCTCGATGTACTTGTGGGGCCCCGAAGGGCACACGGTCTGGTAGAAC  
  
 2521 PheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGlnThr  
 AATTTGGGAGGGCGTCTTACAGGCCTCACTCATATAGATGCCACTTCTATCCCAGA  
 TTAAAACCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTCT  
  
 2581 LysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAlaArg  
 CAAAGCAGAGTGGGAGAACCTCCTACCTGGTAGCGTACCAAGCCACCGTGTGCGCTAAGC  
 GTTTCGTCTACCCCTCTGGAGGAATGGACCATCGCATGGTCTGGCACACGCGAT  
  
 2641 AlaGlnAlaProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLysPro  
 GGGCTCAAGCCCTCCCCATCGTGGGACCAGATGTGGAAGTGGTATCGCCTCAAGC  
 CCCGAGTTCGGGGAGGGGGTAGCACCCCTGGTCTACACCTCACAAACTAACGGAGTTCG  
  
 2701 ThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIleThr  
 CCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGCGCTGTTGAGAATGAAATCA  
 GGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAGT  
  
 2761 LeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluValVal  
 CCCTGACGCACCCAGTCACCAAATACATCATGACATGTCGGCCGACCTGGAGGTGCG  
 GGGACTGCGTGGGTCACTGGTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAGC  
  
 2821 ThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeuSer  
 TCACGAGCACCTGGGTGCTCGTTGGCGCGCTGGCTGCTTGGCCGCGTATTGCGCTGT  
 AGTGCCTCGTGGACCCACGAGCAACGCCGAGGACCGACGAAACCGCGCATAACGGACA  
 ThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIlePro

FIG. 26-3

SUBSTITUTE SHEET

25/63

2881 CAACAGGCTGGTGGTCATA GTGGGCAGGGTGTCTTGTCGGGAAGCCGGCAATCATAC  
GTTGTCCGACGCACCAGTATCACCGTCCCAGCAGAACAGGCCCTCGGCCGTAGTATG

AspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeuPro  
2941 CTGACAGGGAAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGTCTCAGCACTTAC  
GACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTCACGAGAGTCGTGAATG

TyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeuLeu  
3001 CGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTCAAGCAGAACGCCCTCGGCCTCC  
GCATGTAGCTCGTCCCTACTACGAGCGGCTCGTCAAGTGTCTTCCGGGAGCCGGAGG

GlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGlnLys  
3061 TGCAGACCGCGTCCCGTCAGGCAGAGGTTATGCCCTGCTGTCCAGACCAAATGGCAAA  
ACGTCTGGCGCAGGGCAGTCCGTCTCAAATAGCGGGGACGACAGGTCTGGTTGACCGTT

LeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeuAla  
3121 AACTCGAGACCTTCTGGCGAAGCATAATGTGGAACTTCATCAGTGGATACAATACTTGG  
TTGAGCTCTGGAAAGACCCGCTTCGTATACACCTGAAGTAGTCACCTATGTTATGAACC

GlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAlaAla  
3181 CGGGCTTGTCAACGCTGCCCTGGTAACCCGCCATTGCTTCATTGATGGCTTTACAGCTG  
GCCCGAACAGTTGCCGACGGACCATTGGGGCGGTAAAGTAACCTACCGAAAATGTCGAC

ValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrpVal  
3241 CTGTCACCAGCCCCTAAACCCTAGCCAAACCCCTCCTCTAACATATTGGGGGGGTGGG  
GACAGTGGTCGGGTGATTGGTATCGGTTGGGAGGAGAAGTTGTATAACCCCCCCCACCC

AlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAlaGly  
3301 TGGCTGCCAGCTGCCGCCCGGTGCCGCTACTGCCCTTGTGGCGCTGGCTTAGCTG  
ACCGACGGGTCGAGCGGCCGGCCACGGCGATGACGGAAACACCCGCGACCGAACGAC

AlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyrGly  
3361 GCGCCGCCATCGGCAGTGGACTGGGACTGGGAAGGTCTCATAGACATCCTGCAAGGTATG  
CGCGGGCGTAGCCGTACAACCTGACCCCTCAGGAGTATCTGTAGGAACGTCCACATAC

AlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSerThr  
3421 GCGCGGGCGTGGCGGGAGCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCCA  
CGCGCCCGCACCGCCCTCGAGAACACCGTAAGTCTAGTACTGCCACTCCAGGGGAGGT

GluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGlyVal  
3481 CGGAGGACCTGGTCAATCTACTGCCGCCATTCTCGCCCGAGCCCTCGTAGTCGGCG  
GCCTCCTGGACCAGTTAGATGACGGCGGTAGGAGAGCGGGCCTCGGGAGCATGCCGC

ValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrpMet  
3541 TGGTCTGTGCAGCAACTGCGCCGGCACGTTGGCCGGAGGGGGCAGTGCAGTGGAA  
ACCAGACACGTCGTTATGACCGGGCGTGCACCGGGCCCTCCCCGTACGTACCT

AsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrValPro  
3601 TGAACCGGCTGATAGCCTTCGCCCTCCGGGGAAACCATGTTCCCCCACGCACACTACGTGC  
ACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTGGTACAAAGGGGTGCGTATGCACCG

GluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGlnLeu  
3661 CGGAGAGCGATGCGACTGCCCGTCACTGCCATACTCAGCAGCCTACTGTAACCCAGC  
GCCTCTCGCTACGTCGACGGCGCAGTGACGGTATGAGTCGTCGGAGTGCACATTGGTCG

LeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySerTrp  
3721 TCCTGAGGGCAGTGCACCAGTGGATAAGCTGGAGTGTACCACTCCATGCTCCGGTTCC  
AGGACTCCGCTGACGTGGTCACCTATTGAGCCTCACATGGTGAGGTACGAGGCCAAGGA

LeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeuLys  
3781 GGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTAAGACCTGGCTAA  
CCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGTGAATTCTGGACCGATT

AlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyrLys  
3841 AAGCTAAGCTCATGCCACAGCTGCCCTGGATCCCTTGTGTCTGCCAGCGCGGGTATA  
TTCGATTGAGTACGGTGTGACGGACCTAGGGAAACACAGGACGGTGCAGCCATAT

FIG. 26-4

SUBSTITUTE SHEET

26/63

GlyValTrpArgValAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIleThr  
 3901 AGGGGGTCTGGCGAGTGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATCA  
 TCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAGT

GlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMetTrp  
 3961 CTGGACATGTCAAAACGGGACGATGAGGATCGTCGGCTTAGGACCTGCAGGAACATGT  
 GACCTGTACAGTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCTTGACA

SerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAlaPro  
 4021 GGAGTGGGACCTCCCCATTAAATGCCTACACCACGGGCCCCGTACCCCCCTTCCTGCGC  
 CCTCACCTGGAAAGGGTAATTACGGATGTGGTGCCCCGGGACATGGGGGAAAGGACGCG

AsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGlnVal  
 4081 CGAACTACACGTCGCGTATGGAGGGTGTCTGCAGAGGAATATGTGGAGATAAGGCAGG  
 GCTTGATGTGCAAGCGCGATAACCTCCCACAGACGTCTCCTTATACACCTCTATTCCGTCC

GlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGlnVal  
 4141 TGGGGGACTTCACTACGTGACGGGTATGACTACTGACAATCTAAATGCCGTGCCAGG  
 ACCCCTGAAGGTGATGCACTGCCATACTGATGACTGTTAGAGTTACGGCACGGTCC

ProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaProPro  
 4201 TCCCATGCCCGAATTTCACAGAAATTGGACGGGTGCGCCTACATAGGTTGCGCCCC  
 AGGGTAGCGGGCTTAAAAGTGTCTAACCTGCCACGCGGATGTATCAAACGCGGGGG

CysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrProVal  
 4261 CCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTAGAGTAGGACTCCACGAATACCCGG  
 GGACGTTCGGAAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGCC

GlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeuThr  
 4321 TAGGGTCGCAATTACCTTGCAGGCCGAACCGGACGTGGCCGTTGACGTCCATGCTCA  
 ATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGACAACACTGCAGGTACGAGT

AspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerProPro  
 4381 CTGATCCCTCCCATAAACAGCAGAGGCCGGCGAAGGTTGGCGAGGGGATCACCC  
 GACTAGGGAGGGTATATTGTCGTCTCGCCGGCCGCTTCCAACCGCTCCCTAGTGGGG

SerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCysThr  
 4441 CCTCTGTGGCCAGCTCTCGGCTAGCCAGCTATCCGCTCCATCTCAAGGCAACTTGCA  
 GGAGACACCGGTCGAGGAGCCGATCGGTGATAGGCAGGTAGAGAGTCCGTTGAACGT

AlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGlnGlu  
 4501 CCGCTAACCATGACTCCCCCTGATGCTGAGCTATAGAGGCCAACCTCTATGGAGGCAGG  
 GGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTCC

MetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSerPhe  
 4561 AGATGGCGGCAACATCACCAAGGGTTGAGTCAGAAAACAAAGTGGTGAATTCTGGACTCCT  
 TCTACCCGCCGTTGAGTGGTCCAACTCAGTCTTGTACCAACTAACCTGAGGA

AspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeuArg  
 4621 TCGATCCGTTGCGGGAGGAGGACGAGCGGGAGATCTCCGTACCCGAGAAATCCTGC  
 AGCTAGGCGAACACCGCCTCCTGCTGCCCTAGAGGCATGGCGTCTTAGGGAC

LysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnProPro  
 4681 GGAAGTCTGGAGATTGCCAGGGCCTGCCGTTGGCGCGGGACTATAACCCCC  
 CCTTCAGAGCCTCTAACGGGGTCCGGGACGGCAAACCGCGCCGCTGATATTGGGGG

LeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysProLeu  
 4741 CGCTAGTGGAGACGTGGAAAAAGCCGACTACGAACCACTGTGGTCCATGGCTGCGC  
 GCGATCACCTCTGCACCTTTGGCCTGATGCTTGGTGGACACCAGGTACCGACAGGCG

ProProProLysSerProProValProProArgLysLysArgThrValValLeuThr  
 4801 TTCCACCTCAAAGTCCCCCTCTGCGCTCGGAAAGAAGCAGGGACGGTGGTCCCTCA  
 AAGTGGAGGTTTCAGGGAGGACACGGAGGCGGAGCCTTCTCGCCTGCCACCAGGAGT

GluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSerSer

FIG. 26-5

SUBSTITUTE SHEET

27/63

4861 CTGAATCAACCCTATCTACTGCCCTGGCCGAGCTGCCACCAAGAAGCTTGGCAGCTCCT  
 GACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGCTTCGAAACCGTCGAGGA  
 ThrSerGlyIleThrGlyAspAsnThrThrSerSerGluProAlaProSerGlyCys  
 4921 CAACTTCCGGCATTACGGCGACAATACGACAACATCCTCTGAGCCCGCCCCCTGGCT  
 GTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTAGGAGACTCGGGCGGGGAAGACCGA  
 ProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluProGly  
 4981 GCCCCCCCGACTCCGACGCTGAGTCCTATTCCCTCATGCCCGGGCTGGAGGGGGAGCCTG  
 CGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGACCTCCCCCTCGGAC  
 AspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGluAsp  
 5041 GGGATCCGGATCTTAGCGACGGGTATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAGG  
 CCCTAGGCCTAGAATCGCTGCCAGTACCGTGCAGTCATCACTCCGGTTGCGCCTCC  
 ValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAlaAla  
 5101 ATGTCGTGTGCTGCTCAATGCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCCTCG  
 TACAGCACACGACGAGTTACAGAATGAGAACCTGTCCCGTGTGAGCAGTGGGGCACGCGG  
 GluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsnLeu  
 5161 CGGAAGAACAGAAACTGCCCATCAATGCACTAACGAACTCGTTGCTACGTACCACAAATT  
 GCCTTCTTGTCTTGACGGGTAGTTACGTGATTGAGCAACGATGCAGTGGGTGTTAA  
 ValTyrSerThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAspArg  
 5221 TGGTGTATTCCACCACCTCACGCAGTGTGCTGCCAAAGGCAGAAGAAAGTCACATTGACA  
 ACCACATAAGGTGGAGTGCCTCACGAACGGTTCCGTCTTCAGTGTAAACTGT  
 LeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAlaSer  
 5281 GACTGCAAGTTCTGGACAGCCATTACCAAGGACGTACTCAAGGAGGTAAAGCAGCGGCGT  
 CTGACGTTCAAGACCTGTCGGAATGGCCTGCATGAGTCCTCCAATTCTCGCGCCGCA  
 LysValLysAlaAsnLeu  
 5341 CAAAAGTGAAGGCTAACTTG  
 GTTTCACTCCGATTGAAC

FIG. 26-6

28/63

**FIG. 27** Translation of DNA 12f

IlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsn  
 1 CCATATTAAAATCAGGATGTACGTGGGAGGGTCGAACACAGGCTGGAAGCTGCCTGCA  
 GGTATAAATTAGTCCTACATGCACCCCTCCCCAGCTGTGTCCGACCTCGACGGACGT

TrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeu  
 61 ACTGGACGCGGGCGAACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCCT  
 TGACCTGCGCCCCGCTTGCAACGCTAGACCTCTGTCCCTGTCCAGGCTCGAGTCGGGCA

LeuLeuThrThrThrGlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeu  
 121 TACTGCTGACCACACTACACAGTGGCAGGTCCCTCCGTGTTCTCACAAACCTACCAGCCT  
 ATGACGACTGGTGATGTGTCACCGTCCAGGAGGGCACAAGGAAGTGTGGATGGTCGGA

SerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyVal  
 181 TGTCCACCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTGTACGGGG  
 ACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAAACACCTGCACGTCAACATGCC

---

GlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeu  
 241 TGGGGTCAAGCATCGCGTCTGGGCCATTAAGTGGGAGTACGTCGTTCTCCTGTTCTC  
 ACCCCAGTTCGTAGCGCAGGACCCGGTAATTCAACCTCATGCAGCAAGAGGACAAGGAAG

---

LeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGlu  
 301 TGCTTGAGACGCGCGTCTGCTCTGCTTGTGGATGATGCTACTCATATCCCAAGCGG  
 ACGAACGTCTGCGCGCGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCC

-----Overlap with 14i-----  
 AlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeu  
 361 AGGCAGGCTTGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCCGGACGCACGGTC  
 TCCGCCGAAACCTCTGGAGCATTATGAATTACGTCGTAGGGACCAGGCCCTGCGTGCCAG

-----  
 Val  
 421 TTGTATC  
 AACATAG

29/63

**FIG. 28** Translation of DNA 35f

-----Overlap with 39c-----

1 LeuLysGluValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGlu  
 1 TGCTCAAGGAGGGTAAAGCAGCGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGG  
 ACGAGTTCCCTCCAATTCTCGTCGCCGCAGTTTCACTTCCGATTGAACGATAGGCATCTCC

61 AlaCysSerLeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAsp  
 61 AAGCTTGACGCTGACGCCCCACACTCAGCCAAATCCAAGTTGGTTATGGGGCAAAAG  
 TTCGAACGTCGGACTGCGGGGGTGTGAGTCGGTTAGGTTCAAACCAAATACCCGTTTC

121 ValArgCysHisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAspLeuLeu  
 121 ACGTCCGTTGCCATGCCAGAAAGGCCGTAAACCCACATCAACTCCGTGTGAAAGACCTTC  
 TGCAGGCAACGGTACGGTCTTCCGGCATGGGTAGTTGAGGCACACCTTCTGGAAAG

181 GluAspAsnValThrProIleAspThrThrIleMetAlaLysAsnGluValPheCysVal  
 181 TGGAAAGACAATGTAACACCAATAGACACTACCATCATGGCTAAGAACGAGGTTTCTGCG  
 ACCTTCTGTTACATTGTGGTTATCTGTGATGGTAGTACCGATTCTGCTCCAAAAGACGC

241 GlnProGluLysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeuGlyVal  
 241 TTCAAGCCTGAGAAGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTCCCCGATCTGGCG  
 AAGTCGGACTCTCCCCCAGCATTGGTCGAGCAGAGTAGCACAAAGGGCTAGACCCGC

301 ArgValCysGluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAlaValMet  
 301 TGCAGCGTGTGCGAAAAGATGGCTTGTACGACGTGGTTACAAAGCTCCCCTGGCCGTGA  
 ACGCGCACACGCTTTCTACCGAAACATGCTGCACCAATGTTCGAGGGAAACCGGCACT

361 GlySerSerTyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuValGlnAla  
 361 TGGGAAGCTCCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCTCGTGCAAG  
 ACCCTTCGAGGATGCCATAAGTTATGAGTGGCCTGTCGCCAACTTAAGGAGCACGTT

421 TrpLysSerLysLysThrProMetGlyPheSerTyrAspThrArgCysPheAspSerThr  
 421 CGTGGAAAGTCCAAGAAAACCCAAATGGGGTTCTCGTATGATACCCGCTGCTTGACTCCA  
 GCACCTTCAGGTTCTTGGGGTTACCCAAGAGCATACTATGGGCGACGAAACTGAGGT

481 ValThrGluSerAspIleArgThrGluGluAla  
 481 CAGTCACTGAGAGCGACATCCGTACGGAGGAGGCA  
 GTCAGTGACTCTCGCTGTAGGCATGCCCTCCGT

30 / 63

**FIG. 29** Translation of DNA 19g

-----  
1 GluPheLeuValGlnAlaTrpLysSerLysLysThrProMetGlyPheSerTyrAspThr  
GAATTCTCGTGCAGCGTGGAAAGTCCAAGAAAACCCAATGGGGTTCTGTATGATACC  
CTTAAGGAGCACGTTGCACCTTCAGGTTTTGGGGTACCCCAAGAGCATACTATGG  
  
-----Overlap with 35f-----  
61 ArgCysPheAspSerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGln  
CGCTGCTTGACTCCACAGTCAGTGAGAGCGACATCCGTACGGAGGAGGCAATCTACCAA  
GCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCCTCCGTTAGATGGTT  
  
121 CysCysAspLeuAspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeuTyr  
TGTTGTGACCTCGACCCCCAAGCCCCGTGGCCATCAAGTCCCTCACCGAGAGGCTTTAT  
ACAACACTGGAGCTGGGGTTCGGGCGCACCGTAGTTCAAGGGAGTGGCTCTCCGAAATA  
  
181 ValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAla  
GTTGGGGGCCCTTACCAATTCAAGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGCG  
CAACCCCCGGGAGAATGGTTAACGTTCCCCCTCTGACGCCATAGCGTCCACGGCGCG  
  
241 SerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAla  
AGCGGCGTACTGACAACTAGCTGTGGTAACACCCCTCACTGCTACATCAAGGCCGGGCA  
TCGCCGCATGACTGTTGATCGACACCATTGTGGAGTGAACGATGTAGTTCCGGGCCGT  
  
301 AlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuVal  
GCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTGTGGCGACGACTTAGTC  
CGGACAGCTGGCGTCCCAGGGTCTGACGTGGTACGAGCACACACCGCTGCTGAATCAG  
  
361 ValIleCysGluSerAlaGlyValGlnGluAspAlaAla  
GTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGGCGAG  
CAATAGACACTTCGCGCCCCAGGTCTCCTGCGCCGCTC

31/63

**FIG. 30** Translation of DNA 26g

1 GlyGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCys  
 GGGGGGGAGAACTGCGGCTATCGCAGGTGCCGCAGCAGCGTACTGACAACTAGCTGT  
 CCCCCCTCTGACGCCATAGCGTCCACGGCGTTCGCCCATGACTGTTGATCGACA

---

61 GlyAsnThrLeuThrCysTyrIleLysAlaAlaCysArgAlaAlaGlyLeuGln  
 GGTAAACACCCCTCACTTGTACATCAAGGCCGAGCAGCCTGTCGAGCCGAGGGCTCCAG  
 CCATTGTGGGAGTGAACAATGTAGTTCCGGCTCGTCGGACAGCTCGCGTCCGAGGTC

-----Overlap with 19g-----

121 AspCysThrMetLeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyVal  
 GACTGCACCAGCTCGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTC  
 CTGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACACTTCGCGCCCCAG

---

181 GlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaPro  
 CAGGAGGACGCCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCC  
 GTCCTCCTGCGCCGCTCGGACTCTCGGAAGTGCCCTCGATACTGGTCATGAGGCGGGGG

241 ProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsn  
 CCTGGGGACCCCCCACAACCAGAACATCGACTTGGAGCTCATACATCATGCTCCTCCAAC  
 GGACCCCTGGGGGTGTTGGTCTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTG

301 ValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThr  
 GTGTCAGTCGCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACA  
 CACAGTCAGCGGGTGCTGCCGACCTTCAGATGATGGAGTGGGACTGGGATGT

361 ThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeu  
 ACCCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCATGGCTGGCTA  
 TGGGGGGAGCGCTCTCGACGCACCCCTCTGCGTTCTGTGAGGTCAAGGACCGAT

421 GlyAsnIleIleMetPheAlaProThrLeuTrpAla  
 GGCACATAATCATGTTGCCAACACTGTGGCG  
 CCGTTGTATTAGTACAAACGGGGTGTGACACCCGC

**FIG. 31** Translation of DNA 15e

1 GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla  
 CGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGC  
 GCCGCGACCTTCTCCAGATGATGGAGTGGGACTGGGATGTTGGGGAGCGCTCTCG

-----Overlap with 26g-----

61 AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe  
 TGCCTGGGAGACAGCAAGACACACTCCAGTCATGGCTAGGCAACATAATCATGTT  
 ACGCACCCCTCTGCGTTCTGTGAGGTCAAGGACCGATCCGTTGTATTAGTACAA

---

121 AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla  
 TGCCCCCACACTGTGGCGAGGATGATACTGATGACCCATTCTTAGCGTCCTTATAGC  
 ACGGGGGTGTGACACCCGCTCTACTATGACTACTGGTAAAGAAATCGCAGGAATATCG

181 ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu  
 CAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCTGCTACTCCATAGA  
 GTCCCTGGTCGAACCTGTCGGGAGCTAACGCTCTAGATGCCCGACGATGAGGTATCT

241 ProLeuAspLeuProProIleIleGlnArgLeu  
 ACCACTTGATCTACCTCCAATCATTCAAAGACTC  
 TGGTGAAGTGGAGGTTAGTAAGTTCTGAG

32 / 53

## FIG. 32-1 COMBINED ORF OF DNAs 12f through 15e

IlePheLysIleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsn  
 1 CCATATTAAAATCAGGATGTACGTGGAGGGTCAACACAGGCCTGGAAGCTGCCTGCA  
 GGTATAAATTAGTCCTACATGCACCCCTCCCAGCTTGTGTCAGCTCGACGGACGT

TrpThrArgGlyGluArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeu  
 61 ACTGGACGCCGGCGAACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTCAGCCCGT  
 TGACCTGCGCCCCGCTTGCAACGCTAGACCTCTGTCCCTGTCCAGGCTCGAGTCGGGCA

LeuLeuThrThrGlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeu  
 121 TACTGCTGACCACACAGTGGCAGGTCCCTCCGTGTCCTTCACAACCCCTACCAAGCCT  
 ATGACGACTGGTGATGTGTCACCGTCCAGGAGGGCACAAAGGAAGTGTGGATGGTCGGA

SerThrGlyLeuIleHisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyVal  
 181 TGTCACCGGCCTCATCCACCTCCACCAAGAACATTGTGGACGTGCAGTACTGTACGGGG  
 ACAGGTGGCCGGAGTAGGTGGAGGTGGTCTTGTAAACACCTGCACGTCACTAACATGCCCC

GlySerSerIleAlaSerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeu  
 241 TGGGGTCAAGCATCGCGTCTGGGCCATTAAAGTGGAGTACGTCGTTCTCCTGTTCC  
 ACCCCAGTCGTAGCGCAGGACCCGGTAATTCAACCTCATGCAGCAAGAGGACAAGGAAG

LeuAlaAspAlaArgValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGlu  
 301 TGCTTGAGACGCCGCGCTGCTCTGCTTGAGTACGCTACTCATATCCCAAGCGG  
 ACGAACGTCTGCGCGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCC

AlaAlaLeuGluAsnLeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeu  
 361 AGGCGGCTTGAGAACCTCGTAATACTTAATGCACTCCCTGCCGGACGCACGGTC  
 TCCGCCGAAACCTCTGGAGCATTATGAATTACGTCGTAGGGACCAGGCCCTGCGTGCCAG

ValSerPheLeuValPhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGly  
 421 TTGTATCCTCCTCGTGTCTCTGCTTGCATGGTATTGAAGGGTAAGTGGGTGCCCG  
 AACATAGGAAGGAGCACAGAACGAAACGTACCATAAACTCCCATTCAACCCACGGGG

AlaValTyrThrPheTyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGln  
 481 GAGCGGTCTACACCTCTACGGGATGTGGCCTCTGCTCTGCTCTGCTGTTGGCGTTGCC  
 CTCGCCAGATGTGGAAGATGCCCTACACCGGAGAGGAGCAGGACAACCGCAACGGGG

ArgAlaTyrAlaLeuAspThrGluValAlaAlaSerCysGlyGlyValValLeuValGly  
 541 AGCGGGCGTACCGCCTGGACACCGGAGGTGGCCGCGTCGTGTCGCGGTGTTCTCGTCG  
 TCGCCCGATGCGCAGCTGTGCCCTCACCGGCCAGCACACCGCCACAACAAGAGCAGC

LeuMetAlaLeuThrLeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrp  
 601 GGTTGATGGCGCTGACTCTGTCACCATATTACAAGCGCTATATCAGCTGGTGCTTGTGGT  
 CCAACTACCGCAGCTGAGACAGTGGTATAATGTTCGCGATATAGTCGACCACGAACACCA

LeuGlnTyrPheLeuThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsn  
 661 GGCTTCAGTATTTCTGACCAGACTGGAAGCGCAACTGCACGTGGATTCCCCCCTCA  
 CGCAAGTCATAAAAGACTGGTCTCACCTTCGCGTTGACGTGCACACCTAACGGGGAGT

ValArgGlyGlyArgAspAlaValIleLeuLeuMetCysAlaValHisProThrLeuVal  
 721 ACGTCCGAGGGGGCGCGACGCCGTACATCTTACTCATGTGTGCTGTACACCCGACTCTGG  
 TGCAGGCTCCCCCGCGCTGCCAGTAGAATGAGTACACACGACATGTGGCTGAGACC

PheAspIleThrLysLeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSer  
 781 TATTTGACATCACCACAAATTGCTGCTGGCGCTTCGGACCCCTTGGATTCTCAAGCCA  
 ATAAAATGTAGTGGTTAACGACGACCGGAGAAGCCTGGGGAAACCTAACAGAGTCGGT

LeuLeuLysValProTyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAla  
 841 GTTTGCTTAAAGTACCCACTTTGCTGCGCTCAAGGCCTCTCCGGTTCTGCGCGTTAG  
 CAAACGAATTTCATGGGATGAAACACGCGCAGGTTCCGGAAGAGGCCAGACGCGCAATC

ArgLysMetIleGlyGlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThr  
 901 CGCGGAAGATGATCGGAGGCCATTACGTGCAAATGGTCATCATTAAGTTAGGGCGCTTA  
 GCGCCTTCTACTAGCCTCCGTAATGCACGTTACCAAGTAGTAATTCAATCCCCGCGAAT

33/63

GlyThrTyrValTyrAsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArg  
 961 CTGGCACCTATGTTATAACCATCTCACTCCTTCGGGACTGGCGCACAACGGCTTGC  
 GACCGTGGATACAAATATTGGTAGAGTGAGGAGAACGCCGTACCCGCGTGTGCCAACG  
  
 AspLeuAlaValAlaValGluProValValPheSerGlnMetGluThrLysLeuIleThr  
 1021 GAGATCTGGCCGTGGCTGTAGAGCCAGTCGTCTCTCCAAATGGAGACCAAGCTCATCA  
 CTCTAGACCGGCACCGACATCTCGGTACGCAGAAGAGGGTTACCTCTGGTCAGTAGT  
  
 TrpGlyAlaAspThrAlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArg  
 1081 CGTGGGGGGCAGATAACGCCCGTGGGTGACATCATCAACGGCTGCCTGTTCCGCC  
 GCACCCCCCGTCTATGGCGCGCACGCCACTGTAGTTGCCAACGGACAAAGGC  
  
 ArgGlyArgGluIleLeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeu  
 1141 GCAGGGGCCGGAGATACTGCTCGGCCAGCCGATGGAATGGTCTCCAAGGGTGGAGGT  
 CGTCCCCGGCCCTCTATGACGAGCCCCTGGCTACCTTACCAAGAGGTTCCCCACCTCCA  
  
 LeuAlaProIleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThr  
 1201 TGCTGGCGCCCATCACGGCGTACGCCAGCAGACAAGGGCCTCTAGGGTGCATAATCA  
 ACGACCGCGGGTAGTGCCGCATGCCGTCGTCTGTTCCCCGAGGATCCCACGTATTAGT  
  
 SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla  
 1261 CCAGCCTAACTGGCCGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCAACTG  
 GGTCGGATTGACCAGGCCCTGTTGGTCACCTCCACTCCAGGTCTAACACAGTTGAC  
  
 AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAla  
 1321 CTGCCCCAAACCTTCCTGGCAACGTGCATCAATGGGTGTGCTGGACTGTCTACCACGGG  
 GACGGGTTGGAAAGGACCGTTGCACGTAGTTACCCCACACGACCTGACAGATGGTGC  
  
 GlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyrThrAsnValAsp  
 1381 CCGGAACGAGGACCATCGCGTCACCCAGGGCTCTGTCATCCAGATGTATAACCAATGTAG  
 GCCCTGCTCCTGGTAGCGCAGTGGGTTCCCAGGACAGTAGGTCTACATATGGTACATC  
  
 GlnAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThrProCysThrCys  
 1441 ACCAAGACCTTGCTGGCTGGCCCGTCCGCAAGGTAGCCGCTCATGACACCCCTGCAC  
 TGGTTCTGGAACACCCGACCGGGCGAGGCCTCCATCGCGAGTAAGTGGACGTGAA  
  
 GlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIleProValArgArgArg  
 1501 GCGGCTCCTCGGACCTTACCTGGTCACGAGGCACGCCATGTCATTCCCGTGC  
 CGCCGAGGAGCCTGGAAATGGACCAGTGCTCCGTGCGGCTACAGTAAGGCACGCC  
  
 GlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSer  
 1561 GGGGTGATAGCAGGGGCAGCCTGCTGTCGCCCCGGCCATTCTACTTGAAAGGCTCCT  
 CCCCACATCGTCCCCGTCGGACGACAGCGGGCCGGTAAAGGATGAACATTCCGAGGA  
  
 GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys  
 1621 CGGGGGGTCCCGTGTGTCGCCCCGGGGCACGCCGTGGCATATTAGGGCCGCGGT  
 GCCCCCCAGGCACACAGGGGGCGCCCGTGCAGCACCCGTATAAAATCCGGCGCCACA  
  
 ThrArgGlyValAlaLysAlaValAspPheIleProValGluAsnLeuGluThrThrMet  
 1681 GCACCCGTGGAGTGGCTAACGGCGGTGGACTTATCCCTGTGGAGAACCTAGAGACAA  
 CGTGGGCACCTCACCGATTCCGCCACCTGAAATAGGGACACCTCTGGATCTGTGTTGG  
  
 ArgSerProValPheThrAspAsnSerSerProProValValProGlnSerPheGlnVal  
 1741 TGAGGTCCTCGGTGTTCACGGATAACTCCTCTCCACCAGTAGTGCCCCAGAGCTTC  
 ACTCCAGGGGCCACAAGTGCCTATTGAGGAGAGGTGGTCATCACGGGGTCTCGAAGGT  
  
 AlaHisLeuHisAlaProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAla  
 1801 TGGCTCACCTCCATGCTCCCACAGGCAGCGGGAAAAGCACCAAGGTCCGGCTGC  
 ACCGAGTGGAGGTACGAGGGTGTCCGTGCCGTTTCGTGGTCCAGGGCCACGTATAC  
  
 AlaGlnGlyTyrLysValLeuValLeuAsnProSerValAlaAlaThrLeuGlyPheGly  
 1861 CAGCTCAGGGCTATAAGGTGCTAGTACTCAACCCCTGTGCTGCAACACTGGGCTT  
 GTCGAGTCCCGATATTCCACGATCATGAGTTGGGAGACAAACGACGTTGTGACCCGAA  
  
 AlaTyrMetSerLysAlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIle

FIG. 32-2

SUBSTITUTE SHEET

34 / 63

1921 GTGCTTACATGTCCAAGGCTCATGGGATCGATCCTAACATCAGGACCGGGGTGAGAACAA  
CACGAATGTACAGGTTCCGAGTACCCCTAGCTAGGATTGAGTCCTGGCCCCACTCTGTT

1981 ThrThrGlySerProIleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCys  
TTACCACTGGCAGCCCCATCACGTACTCCACCTACGGCAAGTTCCCTGCCGACGGCGGGT  
AATGGTGACCGTCGGGGTAGTGCATGAGGTGGATGCCGTTCAAGGAACGGCTGCCGCCA

2041 SerGlyGlyAlaTyrAspIleIleIleCysAspGluCysHisSerThrAspAlaThrSer  
GCTGGGGGGCGCTTATGACATAATAATTGTGACGAGTGCCACTCCACGGATGCCACAT  
CGAGCCCCCGCGAATACTGTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAA

2101 IleLeuGlyIleGlyThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValVal  
CCATCTGGGCATCGGCACTGTCCTGACCAAGCAGAGACTGCCGGGGCGAGACTGGTTG  
GGTAGAACCGTAGCCGTACAGGAACGGTTCTGACGCCCGCTTGACCAAC

2161 LeuAlaThrAlaThrProProGlySerValThrValProHisProAsnIleGluGluVal  
TGCTGCCACCAGGCCACCCCTCCGGGCTCCGTCACTGTGCCCATCCAACATCGAGGAGG  
ACGAGCGGTGGCGTGGGGAGGCCGAGGCACTGACACGGGTAGGGTTAGCTCCTCC

2221 AlaLeuSerThrThrGlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIle  
TTGCTCTGTCCACCACCGGAGAGATCCCTTTACGGCAAGGCTATCCCCCTCGAAAGTAA  
AACGAGACAGGTGGTGGCCTCTAGGGAAAAATGCCGTTCCGATAGGGGGAGCTTCATT

2281 LysGlyGlyArgHisLeuIlePheCysHisSerLysLysCysAspGluLeuAlaAla  
TCAAGGGGGGGAGACATCTCATCTGTCAATTCAAAGAAGTGCAGCAACTCGCCG  
AGTCCCCCCCCTCTGTAGAGTAGAACAGTAAGTTCTCACGCTGCTGAGCGGC

2341 LysLeuValAlaLeuGlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerVal  
CAAAGCTGGTCGCATTGGGCATCAATGCCGTGGCCTACTACCGCGGTCTGACGTGTCGG  
GTTTCGACCAGCGTAACCGTAGTTACGGCACCGGATGATGGGCCAGAACACTGCACAGGC

2401 IleProThrSerGlyAspValValValAlaThrAspAlaLeuMetThrGlyTyrThr  
TCATCCCGACCAGCGGCGATGTTGTCGTGGCAACCGATGCCCTCATGACCGGCTATA  
AGTAGGGCTGGTCGCCGTACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATAT

2461 GlyAspPheAspSerValIleAspCysAsnThrCysValThrGlnThrValAspPheSer  
CCGGCGACTTCGACTCGGTGATAGACTGCAATACGTGTCACCCAGACAGTCGATTCA  
GGCGCTGAAGCTGAGCCACTATCTGACGTTATGCACACAGTGGGTCTGTCAGCTAAAGT

2521 LeuAspProThrPheThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThr  
GCCTTGACCCCTACCTCACCATTGAGACAATCACGCTCCCCCAGGATGCTGCTCCCGCA  
CGGAACCTGGGATGGAAGTGGTAACCTGTTAGTGCAGGGGTCTACGACAGAGGGCGT

2581 GlnArgArgGlyArgThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGly  
CTCAACGTCGGGGCAGGACTGGCAGGGGGAGCCAGGCATCTACAGATTGTGGCACCGG  
GAGTTGCAGCCCCGTCCCTGACCGTCCCCCTCGGTCCGTAGATGTCTAAACACCGTGGCC

2641 GluArgProSerGlyMetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCys  
GGGAGCGCCCCCTCCGGCATGTTGACTCGTCGTCCCTGTGAGTGCTATGACGCAGGCT  
CCCTCGCGGGGAGGCCGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGA

2701 AlaTrpTyrGluLeuThrProAlaGluThrValArgLeuArgAlaTyrMetAsnThr  
GTGCTGGTATGAGCTCACGCCCGAGACTACAGTTAGGCTACGAGCGTACATGAACA  
CACGAACCATACTGAGTGCAGGGCGTCTGATGTCAATCCGATGCTGCATGTACTTGT

2761 ProGlyLeuProValCysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeu  
CCCCGGGGCTCCCGTGTGCCAGGACCATCTGAATTGGGGAGGGCGTCTTACAGGCC  
GGGGCCCCGAAGGGCACACGGTCTGGTAGAACCTAAACCTCCCGCAGAAATGTCCGG

2821 ThrHisIleAspAlaHisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyr  
TCACTCATATAGATGCCACTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTCCCTT  
AGTGAGTATATCTACGGGTAAAGATAGGGCTGTTCGTCTACCCCTTGGAAAGGAA

2881 LeuValAlaTyrGlnAlaThrValCysAlaArgAlaGlnAlaProProSerTrpAsp  
ACCTGGTAGCGTACCAAGCCACCGTGTGCGTAGGGCTCAAGGCCCTCCCCATCGTGGG  
TGGACCATCGCATGGTGGCACACCGGATCCCGAGTTGGGGAGGGGGTAGCACCC

FIG. 32-3

CONTINUATION SHEET

35/63

2941 GlnMetTrpLysCysLeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeu  
 ACCAGATGTGGAAAGTGTGATTCGCTCAAGCCCACCCATGGGCCAACACCCCTGC  
 TGGTCTACACCTCACAAACTAAGCGGAGTCGGGTGGGAGGTACCCGGTTGGGAGC  
  
 3001 TyrArgLeuGlyAlaValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIle  
 TATACAGACTGGCGCTGTTCAGAATGAAATCACCTGACGCACCCAGTCACCAAATACA  
 ATATGTCTGACCCCGACAAAGTCTTACTTAGTGGACTGCGTGGTCAGTGGTTATGT  
  
 3061 MetThrCysMetSerAlaAspLeuGluValValThrSerThrTrpValLeuValGlyGly  
 TCATGACATGCATGTCGGCGACCTGGAGGTGCGTCACGAGCACCTGGGTGCTCGTTGGCG  
 AGTACTGTACGTACAGCCGCTGGACCTCCAGCAGTGCTGGACCCACGAGCAACCGC  
  
 3121 ValLeuAlaAlaLeuAlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArg  
 GCGTCCTGGCTGCTTGGCCCGTATTGCCTGTCAACAGGGCTGCGTGGTCATAGGGCA  
 CGCAGGACCGACGAAACCGGGCGATAACGGACAGTTGTCGACGCACCAGTATACCCGT  
  
 3181 ValValLeuSerGlyLysProAlaIleIleProAspArgGluValLeuTyrArgGluPhe  
 GGGTCGCTTGTCGGGAAGCCGGCAATCATACCTGACAGGGAACTCCTCTACCGAGAGT  
 CCCAGCAGAACAGGCCCTCGGCCGTAGTATGGACTGTCCTTCAGGAGATGGCTCTCA  
  
 3241 AspGluMetGluGluCysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAla  
 TCGATGAGATGAAAGAGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCG  
 AGCTACTCTACCTCTCACGAGAGTCGTGAATGGCATGTAGCTCGTCCCTACTACGAGC  
  
 3301 GluGlnPheLysGlnLysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluVal  
 CCGAGCAGTTCAAGCAGAACGGCCCTCGGCCTCCCTGAGACCCGCTCCCGTCAGGCAGAGG  
 GGCTCGTCAAGTTGCTCTCCGGGAGCCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCC  
  
 3361 IleAlaProAlaValGlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMet  
 TTATCGCCCCCTGCTGTCCAGACCAACTGGAAAAACTCGAGACCTTCTGGCGAAGCATA  
 AATAGCGGGGACGACAGGTCTGGTTGACCGTTTGAGCTCTGGAAGACCCGTTCGTAT  
  
 3421 TrpAsnPheIleSerGlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnPro  
 TGTGGAACTTCATCAGTGGGATACAATACTTGGCGGGCTGTCAACGCTGCCCTGGTAACC  
 ACACCTTGAAGTAGTCACCCATGTTATGAACCGCCGAACAGTTGCGACGGACCATTGG  
  
 3481 AlaIleAlaSerLeuMetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGln  
 CCGCCATTGCTTCATTGATGGCTTTACAGCTGCTGTCACCAGCCCACAACTAGCC  
 GGCGGTAACGAAGTAACCTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTATCGG  
  
 3541 ThrLeuLeuPheAsnIleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAla  
 AAACCCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCAGCTGCCGCCGGTG  
 TTTGGGAGGAAGTTGTATAACCCCCCACCACCGACGGTCAGCGGGGCCAC  
  
 3601 AlaThrAlaPheValGlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGly  
 CCGCTACTGCCTTGTGGCGCTGGCTTAGCTGGCGCCATCGCAGTGTGGACTGG  
 GCGATGACGGAAACACCCCGACCGAATCGACCGCGGGTAGCCGTACAACCTGACC  
  
 3661 LysValLeuIleAspIleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAla  
 GGAAGGTCCTCATAGACATCCTGCAAGGGTATGGCGCGGTGGAGCTTTGTGG  
 CCTTCCAGGAGTATCTGAGAACGTCACCAACCGCCCTCGAGAACAC  
  
 3721 PheLysIleMetSerGlyGluValProSerThrGluAspLeuValAsnLeuLeuProAla  
 CATTCAAGATCATGAGCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCG  
 GTAAAGTTCTAGTACTGCCACTCCAGGGGAGGTGCGCTCGGACCAAGTTAGATGACGGGC  
  
 3781 IleLeuSerProGlyAlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHis  
 CCATCCTCTCGCCCCGGAGCCCTCGTAGTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGC  
 GGTAGGGAGAGCGGGCCTCGGGAGCATCAGCCGACCAAGACACGTCGTTATGACGGCG  
  
 3841 ValGlyProGlyGluGlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArg  
 ACGTTGGCCCGGGCAGGGGGCAGTGCAGTGGATGAACGGCTGATAGCCTTCGCCTCCC  
 TGCAACCGGGCCCGCTCCCCCGTCACGTCACCTACTGGCCGACTATCGGAAGCGGAGGG  
  
 GlyAsnHisValSerProThrHisTyrValProGluSerAspAlaAlaArgValThr

FIG. 32-4

36/63

3901 GGGGGAAACCATTTCCCCCACGCCTACGTGCCGGAGAGCGATGCAGCTGCCCGCTCA  
CCCCCTGGTACAAAGGGGGTGCCTGATGCACGGCCTCTCGCTACGTGACGGCGCAGT

3961 AlaIleLeuSerSerLeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSer  
CTGCCATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAA  
GACGGTATGAGTCGTCGGAGTGACATTGGTCGAGGACTCCGCTGACGTGGTCACCTATT

4021 SerGluCysThrThrProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCys  
GCTCGGGAGTGTACCACTCCATGCTCCGGTCTGGCTAAGGGACATCTGGGACTGGATAT  
CGAGCCTCACATGGTGAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCGTGACCTATA

4081 GluValLeuSerAspPheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGly  
GCGAGGTGTTGAGCGACTTTAACGACTGGCTAAAGCTAAGCTCATGCCACAGCTGCCTG  
CGCTCCACAACACTCGCTGAAATTCTGGACCGATTTCGAGTACGGTGTGACGGAC

4141 IleProPheValSerCysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMet  
GGATCCCCTTGTCCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATCA  
CCTAGGGGAAACACAGGACGGTCGCCCATATTCCCCAGACCGCTCACCTGCCGTAGT

4201 HisThrArgCysHisCysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArg  
TGCACACTCGCTGCCACTGTGGAGCTGAGATCACTGGACATGTCAAAACGGGACGATGA  
ACGTGTGAGCGACGGTGACACCTGACTCTAGTGACCTGTACAGTTTGCCTGCTACT

4261 IleValGlyProArgThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyr  
GGATCGTCGGTCCTAGGACCTGCAGGAACATGTGGAGTGGACCTTCCCCATTATGCCT  
CCTAGCAGCCAGGATCCTGGACGTCTGTACACCTCACCTGGAAAGGGGTAATTACGGA

4321 ThrThrGlyProCysThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgVal  
ACACCACGGGCCCTGTACCCCCCTCCTGCCAGCGGGTATAAGGGAGCTACACGTTCGCGCTATGGAGGG  
TGTGGTGCCCCGGGACATGGGGGGAAAGGACGCCGTTGATGTGCAAGCGCGATACTCCCC

4381 SerAlaGluGluTyrValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMet  
TGTCTGCAGAGGAATATGTGGAGATAAGGCAGGTGGGGACTTCCACTACGTGACGGGTA  
ACAGACGTCTCCTTATACACCTCTATTCCGTCACCCCTGAAGGTGATGCACTGCCCAT

4441 ThrThrAspAsnLeuLysCysProCysGlnValProSerProGluPhePheThrGluLeu  
TGACTACTGACAATCTCAAATGCCGTGCCAGGTCCCCTGCCAGCGGGTAAAGGTGCTTA  
ACTGATGACTGTAGAGTTACGGGCACGGTCCAGGGTAGCGGGCTAAAAAGTGTCTTA

4501 AspGlyValArgLeuHisArgPheAlaProProCysLysProLeuLeuArgGluGluVal  
TGGACGGGGTGCCTACATAGGTTGCGCCCCCTGCAAGCCCTGCTGCCGGAGGAGG  
ACCTGCCCCACGCCGATGTATCAAACGCCGGGGACGTTGGGAACGACGCCCTCCTCC

4561 SerPheArgValGlyLeuHisGluTyrProValGlySerGlnLeuProCysGluProGlu  
TATCATTCAAGAGTAGGACTCCACGAATAACCGGTAGGTCGCAATTACCTGCGAGCCCG  
ATAGTAAGTCTCATCCTGAGGTGCTTATGGGCCATCCAGCGTTAATGGAACGCTCGGGC

4621 ProAspValAlaValLeuThrSerMetLeuThrAspProSerHisIleThrAlaGluAla  
AACCGGACGTGGCCGTGTTGACGCCATGCTCACTGATCCCTCCATATAACAGCAGAGG  
TTGGCCTGCACCCGACAACCTGAGGTGACTAGGGAGGGTATATTGCGTCTCC

4681 AlaGlyArgArgLeuAlaArgGlySerProProSerValAlaSerSerAlaSerGln  
CGGCCGGCGAAGGTTGGCAGGGGATCACCCCTCTGTGGCCAGCTCCTGGCTAGCC  
GCCGGCCCCGCTCCAACCGCTCCCTAGTGGGGGGAGACACCGGTCGAGGAGCCGATCGG

4741 LeuSerAlaProSerLeuLysAlaThrCysThrAlaAsnHisAspSerProAspAlaGlu  
AGCTATCCGCTCCATCTCTCAAGGCAACTGCACCGCTAACCATGACTCCCTGATGCTG  
TCGATAGGCGAGGTAGAGAGTTCCGTTGAACGTGGCGATTGGTACTGAGGGGACTACGAC

4801 LeuIleGluAlaAsnLeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGlu  
AGCTCATAGAGGCCAACCTCCTATGGAGGCAGGAGATGGCGGGCAACATCACCAGGGTTG  
TCGAGTATCTCCGGTTGGAGGATACCTCCGCTCCTACCCGCCGTTGATGGTCCCAAC

4861 SerGluAsnLysValValIleLeuAspSerPheAspProLeuValAlaGluGluAspGlu  
AGTCAGAAAACAAAGTGGTGATTCTGGACTCCTCGATCCGCTTGTGGCGGGAGGAGGACG  
TCAGTCTTTGTTCAACCAACTAAGACCTGAGGAAGCTAGGCGAACACCGCCTCCTGC

FIG. 32-5

37/63

ArgGluIleSerValProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeu  
 4921 AGCGGGAGATCTCCGTACCCGCAGAAATCCTGCCGAAGTCTCGGAGATTGCCAGGCC  
 TCGCCCTCTAGAGGCATGGCGTCTTAGGACGCCCTCAGAGCCTCAAGCGGGTCCGGG

ProValTrpAlaArgProAspTyrAsnProProLeuValGluThrTrpLysLysProAsp  
 4981 TGCCCCTTTGGCGCGGCCGGACTATAACCCCCGCTAGTGGAGACGTGGAAAAAGCCCG  
 ACGGGCAAACCGCGCCGCCCTGATATTGGGGGGCATCACCTCTGCACCTTTTCGGGC

TyrGluProProValValHisGlyCysProLeuProProLysSerProProValPro  
 5041 ACTACGAACCACCTGTGGTCCATGGCTGTCCACCTCAAAGTCCCTCCTGTGC  
 TGATGCTTGGTGGACACCAGGTACCGACAGGCGAAGGTGGAGGTTCAGGGAGGACACG

ProProArgLysLysArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAla  
 5101 CTCCGCCTCGGAAGAACGCGACGGTGGCCTCACTGAATCAACCCATCTACTGCCTTGG  
 GAGGCGGAGCCTTCGCCACCAGGAGTGACTTAGTGGATAGATGACGGAACC

GluLeuAlaThrArgSerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThr  
 5161 CCGAGCTGCCACCAGAACGCTTGGCAGCTCCCACTTCCGGCATACGGCGACAATA  
 GGCTCGAGCGGTGGCTTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTAT

ThrThrSerSerGluProAlaProSerGlyCysProProAspSerAspAlaGluSerTyr  
 5221 CGACAAACATCCTCTGAGCCCCCCCCTCTGGCTGCCCCCGACTCCGACGCTGAGTCCT  
 GCTGTTGTAGGAGACTCGGGGGGGAAAGACCGACGGGGGGCTGAGGCTGCGACTCAGGA

SerSerMetProProLeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrp  
 5281 ATTCCCTCCATGCCCCCCCTGGAGGGGGAGCCTGGGATCCGGATCTTAGCGACGGGTCA  
 TAAGGAGGTACGGGGGGACCTCCCCCTCGGACCCCTAGGCCTAGAATCGCTGCCAGTA

SerThrValSerSerGluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSer  
 5341 GGTCAACGGTCAGTAGTGAGGCCAACCGGGAGGATGTCGTGCTGCTCAATGTCTTACT  
 CCAGTTGCCAGTCATCACTCCGGTTGCGCCTCCTACAGCACACGACGAGTTACAGAATGA

TrpThrGlyAlaLeuValThrProCysAlaAlaGluGluGlnLysLeuProIleAsnAla  
 5401 CTTGGACAGGCGCACTCGTCACCCCGTGCACCGGGAAAGAACAGAAACTGCCATCAATG  
 GAACCTGTCGCGTGAGCAGTGGGACCGGGCCTTCTTGCTTTGACGGGTAGTTAC

LeuSerAsnSerLeuLeuArgHisHisAsnLeuValTyrSerThrThrSerArgSerAla  
 5461 CACTAAGCAACTCGTTGCTACGTACACACAATTGGTATTCCACCTCACGCAGTG  
 GTGATTGTTGAGCAACGATGCAGTGGTAAACCACATAAGGTGGAGTGCACGTAC

CysGlnArgGlnLysLysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGln  
 5521 CTTGCCAAAGGCAGAACAGAAAGTCACATTGACAGACTGCAAGTCTGGACAGCCATTACC  
 GAACGGTTCCGTCTTCAGTGTAAACTGTCTGACGTTCAAGACCTGTCGGTAATGG

AspValLeuLysGluValLysAlaAlaAlaSerLysValLysAlaAsnLeuLeuSerVal  
 5581 AGGACGTACTCAAGGAGGTTAAAGCAGCGCGTCAAAAGTGAAGGCTAACTTGCTATCCG  
 TCCTGCATGAGTTCTCCAATTGTCGCGCAGTTTCACTCCGATTGAACGATAGGC

GluGluAlaCysSerLeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAla  
 5641 TAGAGGAAGCTTGACGCCACTCAGCCAAATCCAAGTTGGTTATGGGG  
 ATCTCCTCGAACGTCGGACTGCGGGGTGTGAGTGGTTAGGTTCAAACCAATACCCC

LysAspValArgCysHisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAsp  
 5701 CAAAAGACGTCCGTTGCCATGCCAGAACAGCGTAACCCACATCAACTCCGTGTGGAAAG  
 GTTTCTGCAGGCAACGGTACGGTCTTCCGGCATGGGTAGTTGAGGCACACCTTC

LeuLeuGluAspAsnValThrProIleAspThrThrIleMetAlaLysAsnGluValPhe  
 5761 ACCTTCTGGAAGACAATGTAACACCAATAGACACTACCATGCTAAGAACGAGGTTT  
 TGGAAAGACCTTCTGTTACATTGTGGTATCTGTGATGGTAGTACCGATTCTGCTCCAAA

CysValGlnProGluLysGlyArgLysProAlaArgLeuIleValPheProAspLeu  
 5821 TCTGCGTTCAGCCTGAGAAGGGGGTCGTAAGCCAGCTCGTCTCATCGTGTCCCCGATC  
 AGACGCAAGTCGGACTCTCCCCCAGCATTGGTCGAGCAGAGTAGCACAAGGGGCTAG

GlyValArgValCysGluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAla

FIG. 32-6

5881 TGGGCGTGCACGCGCACACGCTTCATACGAAACATGCTGCACCAATGTTGAGGGGAACC  
 ACCCGCACGCGCACACGCTTCATACGAAACATGCTGCACCAATGTTGAGGGGAACC  
 ValMetGlySerSerTyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuVal  
 5941 CCGTGATGGGAAGCTCTACGGATTCCAATACTCACCAGGACAGCGGGTTGAATTCTCG  
 GGCACCTACCCCTCGAGGATGCCTAAGGTTATGAGTGGCCTGTCGCCAACCTAACGGAGC  
 GlnAlaTrpLysSerLysSerLysThrProMetGlyPheSerTyrAspThrArgCysPheAsp  
 6001 TGCAAGCGTGGAAAGTCCAAGAAAACCCCAATGGGGTCTCGTATGATAACCGCTGCTTGTG  
 ACGTTGCGCACCTCAGGTCTTTGGGGTACCCCAAGAGCATACTATGGCGACGAAAC  
 SerThrValThrGluSerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeu  
 6061 ACTCCACAGTCACTGAGAGCGACATCCGTACGGAGGAGCAATCTACCAATGTTGTGACC  
 TGAGGTGTCAGTGACTCTCGCTGTAGGCATGCCTCCGTTAGATGGTTACAACACTGG  
 AspProGlnAlaArgValAlaIleLysSerLeuThrGluArgLeuTyrValGlyGlyPro  
 6121 TCGACCCCCAAGCCCGCGTGGCCATCAAGTCCCTCACCGAGAGGCTTATGTTGGGGGCC  
 AGCTGGGGTTCGGCGCACCGTAGTTCAGGGAGTGGCTCTCCGAAATACAACCCCCGG  
 LeuThrAsnSerArgGlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeu  
 6181 CTCTTACCAATTCAAGGGGGAGAACTGCGGCTATCGCAGGTGCCGCGAGCGGGTAC  
 GAGAATGGTTAAGTCCCCCTCTGACGCCGATAGCGTCCACGGCGCGCTGCCGCATG  
 ThrThrSerCysGlyAsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAla  
 6241 TGACAACTAGCTGTGGTAACACCCCTCACTTGCTACATCAAGGCCCAGCCTGTCGAG  
 ACTGTTGATCGACACCATTGTGGAGTGAACGATGTAGTTCCGGGCCGTCGGACAGCTC  
 AlaGlyLeuGlnAspCysThrMetLeuValCysGlyAspAspLeuValValIleCysGlu  
 6301 CCGCAGGGCTCCAGGACTGCACCATGCTGTGTGGCAGCAGCTAGTCGTTATCTGTG  
 GGCGTCCCGAGGTCTGACGTGGTACGAGCACACACCGCTGCTGAATCAGCAATAGACAC  
 SerAlaGlyValGlnGluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArg  
 6361 AAAGCGCGGGGGTCCAGGAGGACCGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCA  
 TTTCGCGCCCCCAGGTCTCGCCGCTCGACTCTCGGAAGTGCCTCCGATACTGGT  
 TyrSerAlaProProGlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSer  
 6421 GGTACTCCGCCCCCCCCTGGGACCCCCCACAACCAGAACGACTTGGAGGCTATAACAT  
 CCATGAGGCGGGGGGACCCCTGGGGGTGTTGGTCTATGCTAACCTCGAGTATTGTA  
 CysSerSerAsnValSerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThr  
 6481 CATGCTCCTCCAACGTGTCAGTCGCCCCACGACGGCGCTGGAAAGAGGGCTACTACCTCA  
 GTACGAGGAGGTGACAGTCAGCGGGTGCTGCCGACCTTCTCCAGATGATGGAGT  
 ArgAspProThrThrProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProVal  
 6541 CCCGTGACCCCTACAACCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAG  
 GGGCACTGGGATGTTGGGGGAGCGCTCTCGACGCACCCCTCTGCGTTCTGTGAGGTC  
 AsnSerTrpLeuGlyAsnIleIleMetPheAlaProThrLeuTrpAlaArgMetIleLeu  
 6601 TCAATTCCCTGGCTAGGCAACATAATCATGTTGCCACACTGTGGGCGAGGATGATAC  
 AGTTAAGGACCGATCCGTTATTAGTACAAACGGGGTGTGACACCCGCTCCTACTATG  
 MetThrHisPhePheSerValLeuIleAlaArgAspGlnLeuGluGlnAlaLeuAspCys  
 6661 TGATGACCCATTCTTGTAGCGTCTTATAGCCAGGGACCAGCTGAACAGGCCCTCGATT  
 ACTACTGGGTAAAGAAATCGCAGGAATATCGGTCCCTGGTCGAACCTGTCCGGAGCTAA  
 GluIleTyrGlyAlaCysTyrSerIleGluProLeuAspLeuProProIleIleGlnArg  
 6721 GCGAGATCTACGGGGCCTGCTACTCCATAGAACCAACTGATCTACCTCCAATCATTCAA  
 CGCTCTAGATGCCCGGACGATGAGGTATTTGGTGAACTAGATGGAGGTAGTAAGTT  
 Leu  
 6781 GACTC  
 CTGAG

FIG. 32-7

39/63

## FIG. 33 LEGEND

Lane Number	Chimp Reference Number	Infection Type	Sample date (days) (0=inoculation day)	ALT (alanine aminotransferase level in sera) μM/ml)
1	1	NANB	0	9
2	1	NANB	76	71
3	1	NANB	118	19
4	1	NANB	154	N/A
5	2	NANB	0	5
6	2	NANB	21	52
7	2	NANB	73	13
8	2	NANB	138	N/A
9	3	NANB	0	8
10	3	NANB	43	205
11	3	NANB	53	14
12	3	NANB	159	6
13	4	NANB	-3	11
14	4	NANB	55	132
15	4	NANB	83	N/A
16	4	NANB	140	N/A
17	5	HAV	0	4
18	5	HAV	25	147
19	5	HAV	40	18
20	5	HAV	268	5
21	6	HAV	-8	N/A
22	6	HAV	15	106
23	6	HAV	41	10
24	6	HAV	129	N/A
26	7	HAV	0	7
27	7	HAV	22	83
28	7	HAV	115	5
29	7	HAV	139	N/A
30	8	HAV	0	15
31	8	HAV	26	130
32	8	HAV	74	8
33	8	HAV	205	5
34	9	HBV	-290	N/A
35	9	HBV	379	9
36	9	HBV	435	6
37	10	HBV	0	8
38	10	HBV	111-118 (pool)	96-156 (pool)
39	10	HBV	205	9
40	10	HBV	240	13
41	11	HBV	0	11
42	11	HBV	28-56 (pool)	8-100 (pool)
43	11	HBV	169	9
44	11	HBV	223	10

40 / 63

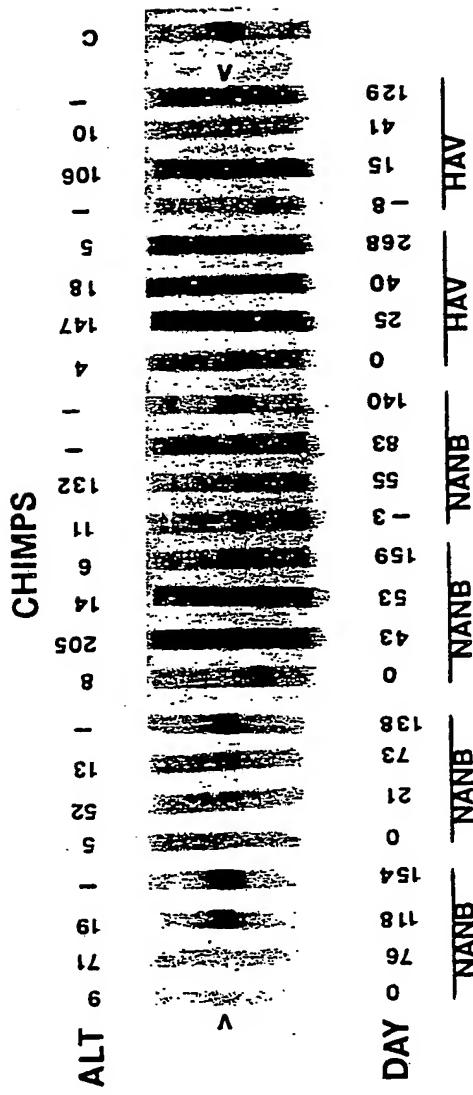


FIG. 33-1

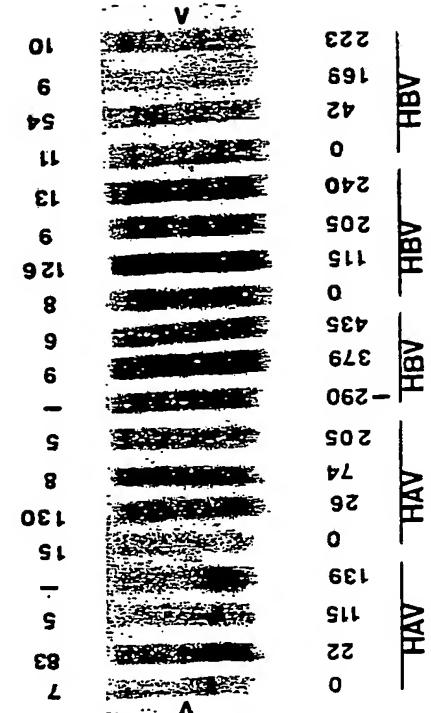


FIG. 33-2

## FIG. 34 LEGEND

Lane Number	Patient Reference Number	Diagnosis	ALT Level (m <sub>g</sub> /ml)
1	1 <sup>1</sup>	NANB	1354
2	11	NANB	31
3	21	NANB	14
4	21	NANB	79
5	21	NANB	26
6	31	NANB	78
7	31	NANB	87
8	31	NANB	25
9	41	NANB	60
10	41	NANB	13
11	51	NANB	298
12	51	NANB	101
13	61	NANB	474
14	61	NANB	318
15	71	NANB	20
16	71	NANB	163
17	81	NANB	44
18	81	NANB	50
19	9	NANB	N/A
20	10	NANB	N/A
21	11	NANB	N/A
22	12	Normal	N/A
23	13	Normal	N/A
24	14	Normal	N/A
26	30174	Normal	N/A
27	30105	Normal	N/A
28	30072	Normal	N/A
29	30026	Normal	N/A
30	30146	Normal	N/A
31	30250	Normal	N/A
32	30071	Normal	N/A
33	15	AcuteHAV	N/A
34	16	AcuteHAV	N/A
35	17	AcuteHAV	N/A
36	18	AcuteHAV	N/A
37	48088	AcuteHAV	N/A
38	47288	AcuteHAV	N/A
39	47050	AcuteHAV	N/A
40	46997	AcuteHAV	N/A
41	19	Convalescent HBV	N/A
42	20	(anti-HBSag+ve;	N/A
43	21	anti-HBCag+ve)	N/A
44	22	(anti-HBSag+ve;	N/A
45	23	anti-HBCag+ve)	N/A
46	24	(anti-HBSag+ve;	N/A
47	25	anti-HBCag+ve)	N/A
48	26	(anti-HBSag+ve;	N/A
49	27	anti-HBSag+ve)	N/A

<sup>1</sup> Sequential serum samples were assayed from these patients

42/63

FIG. 34-1

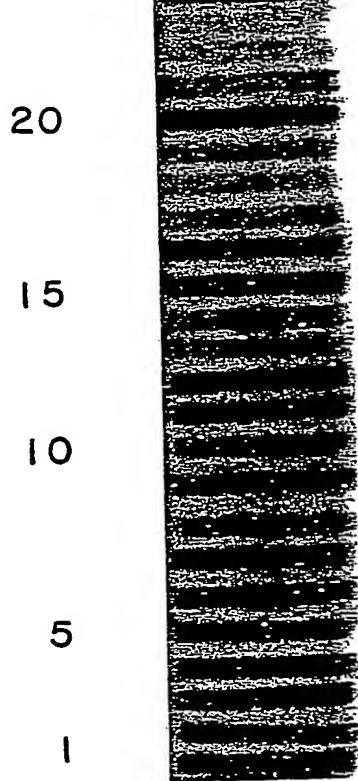
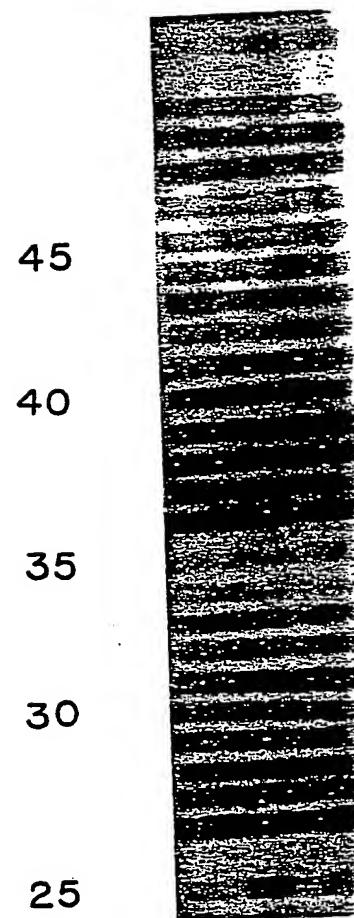
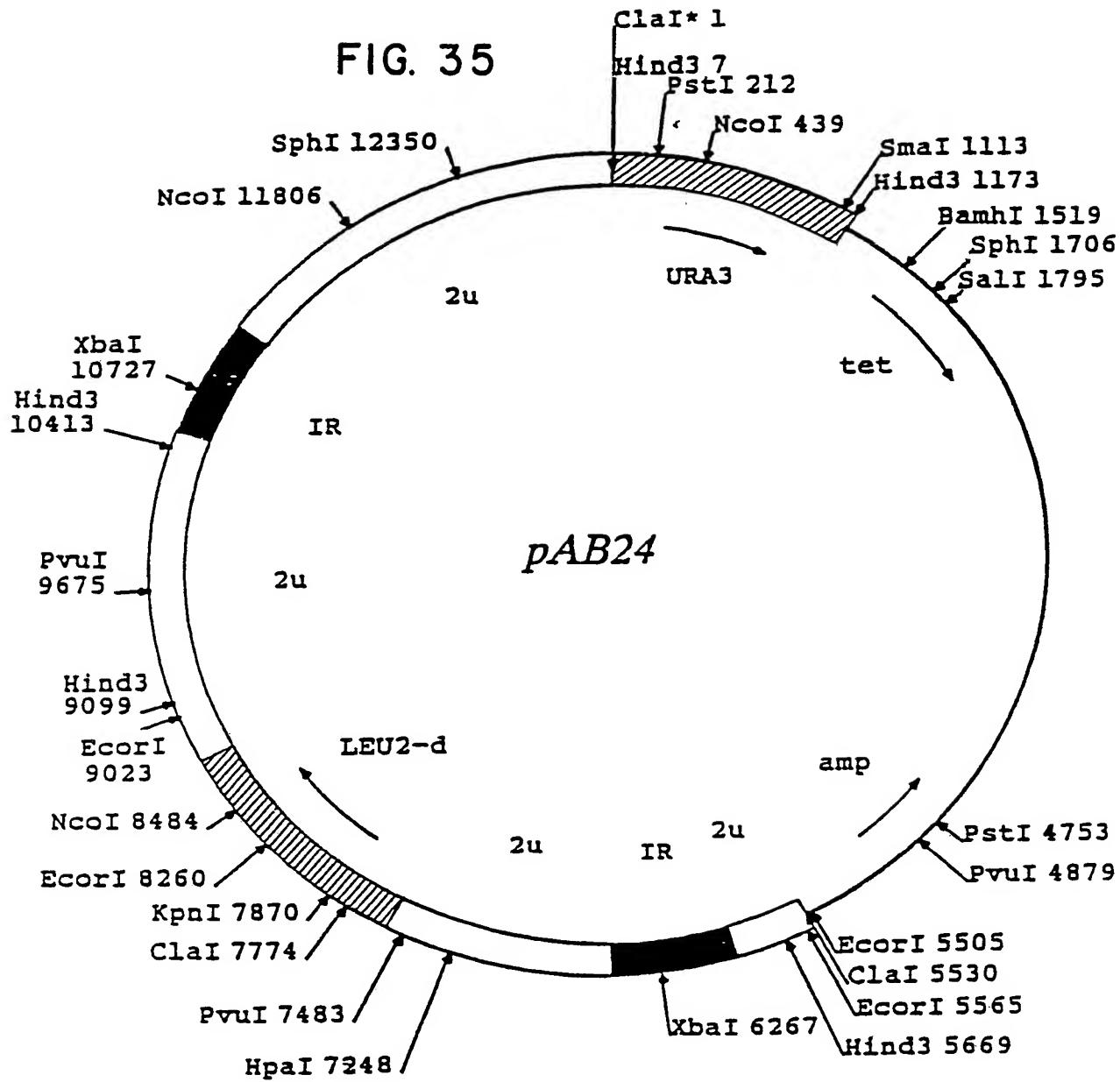


FIG. 34-2



43/63

FIG. 35



44/63

## FIG. 36-1 COOH-terminus of SOD-C100 Fusion Polypeptide

-----SOD-----COOH] [--adaptor----] [NANBHPolypeptide>

1 AlaCysGlyValIleGlyIleAlaGlnAsnLeuGlyIleArgAspAlaHisPheLeuSer  
 GCTTGTTGGTGAATTGGGATGCCAGAATTGGGAAATCGGGATGCCACTTCTATCC  
 CGAACACCACATTAACCCTAGCGGGTCTAACCCCTAACGCCTACGGGTGAAAGATAGG

\* >>>>>>>>>>>>>  
 61 GlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCys  
 CAGACAAAGCAGAGTGGGGAGAACCTTCCTACCTGGTAGCGTACCAAGCCACCGTGTGC  
 GTCTGTTCTCGTCTCACCCCTCTGGAAAGGAATGGACCATCGCATGGTTCGGTGGCACAGC

121 AlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeu  
 GCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAAGTGTGATTGCCCTC  
 CGATCCGAGTCGGGGAGGGTAGCACCCCTGGTCTACACCTTCACAAACTAACGGAG

181 LysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGlu  
 AAGCCCACCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAAATGAA  
 TTCGGGTGGGAGGTACCCGGTTGTGGGGACGATAATGCTGACCCGCGACAAGTCTTACTT

241 IleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGlu  
 ATCACCCCTGACGCACCCAGTCACCAAATACATCATGACATGTCGGCCGACCTGGAG  
 TAGTGGGACTGCGTGGGTCACTGGTTATGTAGTACTGTACAGCCGCTGGACCTC

301 ValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCys  
 GTCGTCACGAGCACCTGGGTGTCGTTGGCGCGTCTGGCTTGGCCGCGTATTG  
 CAGCAGTGCTCGTGGACCCACGAGCAACCGCCGAGGACCGACGAAACCGGCGCATAACG

361 LeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIle  
 CTGTCACACAGGCTGCGTGGTCATAGTGGCAGGGTCGTCTGGCTCCGGGAAGCCGGCAATC  
 GACAGTTGTCCGACGCAACAGTATCACCCGCTCCAGCAGAACAGGCCCTCGGCCGTTAG

421 IleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHis  
 ATACCTGACAGGGAAAGTCCTCTACCGAGAGTCGATGAGATGGAAGAGTGCTCTCAGCAC  
 TATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCACCTCTCACGAGAGTCGTG

481 LeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGly  
 TTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTCAAGCAGAAGGCCCTCGGC  
 AATGGCATGTAGCTCGTCCCTACTACGAGCGGCTCGTCAAGTTGCTTCCGGGAGGCCG

541 LeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrp  
 CTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATGCCCTGCTGTCAGACCAACTGG  
 GAGGACGTCTGGCGCAGGGCAGTCCGTCCTAACAGCAGGACAGGTCTGGTTGACC

601 GlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyr  
 CAAAAACTCGAGACCTCTGGCGAAGCATATGTGAACTTCATCAGTGGGATACAATAC  
 GTTTTGAGCTCTGGAAGACCCGCTCGTATACACCTTGAAGTAGTCACCCCTATGTTATG

661 LeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThr  
 TTGGCGGGCTTGTCAACGCTGCCGTGGTAACCCCGCATTGCTTCATTGATGGCTTTACA  
 AACCGCCCCAACAGTTGCGACGGACCATTGGGGCGTAACGAAGTAACCTACGGAAAATGT

721 AlaAlaValThrSerProLeuThrSerGlnThrLeuLeuPheAsnIleLeuGlyGly  
 GCTGCTGTCAACAGCCCCTAACCAACTAGCCAAACCCCTCTCAACATATTGGGGGGGG  
 CGACGACAGTGGTCGGGTGATTGGTATCGGTTGGGAGGAGAAGTTGTATAACCCCCCCC

781 TrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeu  
 TGGGTGGCTGCCAGCTGCCGCCCCGGTGCCTACTGCTTGTGGCGCTGGCTTA  
 ACCCACCGACGGGTGAGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAAT

841 AlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGly  
 GCTGGCGCCGCCATCGGCAGTGGACTGGGAAGGTCTCATAGACATCCTGCAAGGG

45/63

CGACCGCGGCGGTAGCCGTACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCC

901 TyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValPro  
TATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAGATCATGAGCGGGTGAGGTCCCC  
ATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGG

961 SerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValVal  
TCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGAGCCCTCGTAGTC  
AGGTGCCTCCTGGACCAGTTAGATGACGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAG

1021 GlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGln  
GGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAG  
CCGCACCAGACACGTGTTATGACGCGGCCGTGCAACCGGGCCGTCACGTC

<<<<<<<<<<< NANBH ] [---extra  
1081 TrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProValHisHis  
TGGATGAACCGGCTGATAGCCTCGCCTCCGGGGAACATGTTCCCATCAT  
ACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGTCAAGGTAGTA

-----]  
LysArgOP  
1141 AAGCGTTGACGCTCCCTACGGGTGGACTGTGGAGAGACAGGGCACTGCTAAGGCCAAAT  
TTCGCAACTGCGAGGGATGCCACCTGACACCTCTGTCCGTGACGATTCCGGTTA

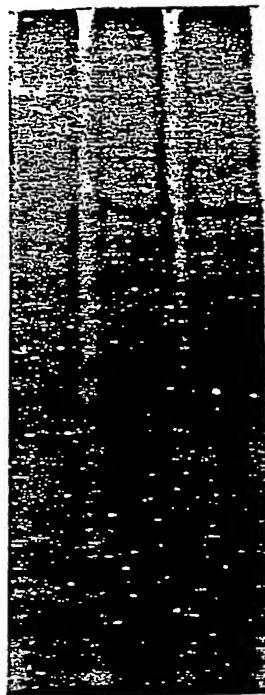
1201 CTCAGCCATGCATCGAGGGGTACAATCCGTATGGCCAACAACACTAGCGCGTACGTAAAGTC  
GAGTCGGTACGTAGCTCCCCATGTTAGGCATACCGGTGTTGATCGCGCATGCATTCAAG

1261 TCCTTCTCGATGGTCCATACCTTAGATGCGTTAGCATTAAATCGAATT  
AGGAAAAGAGCTACCAGGTATGGAATCTACGCAATCGTAATTAGGCTTAAG

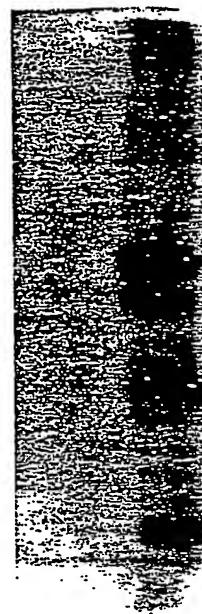
FIG. 36-2

46/63

1 2 3



1 2

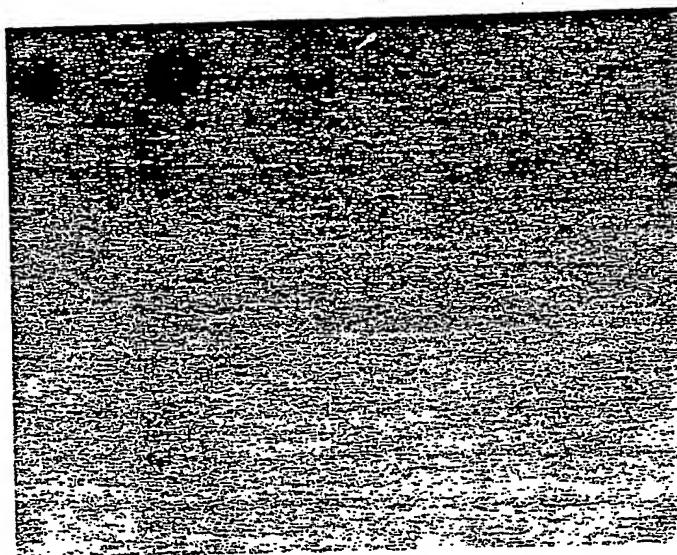


**FIG. 37 b**

**FIG. 37 a**

1 2 3

A



**FIG. 39**

47/63

1 2 3 4

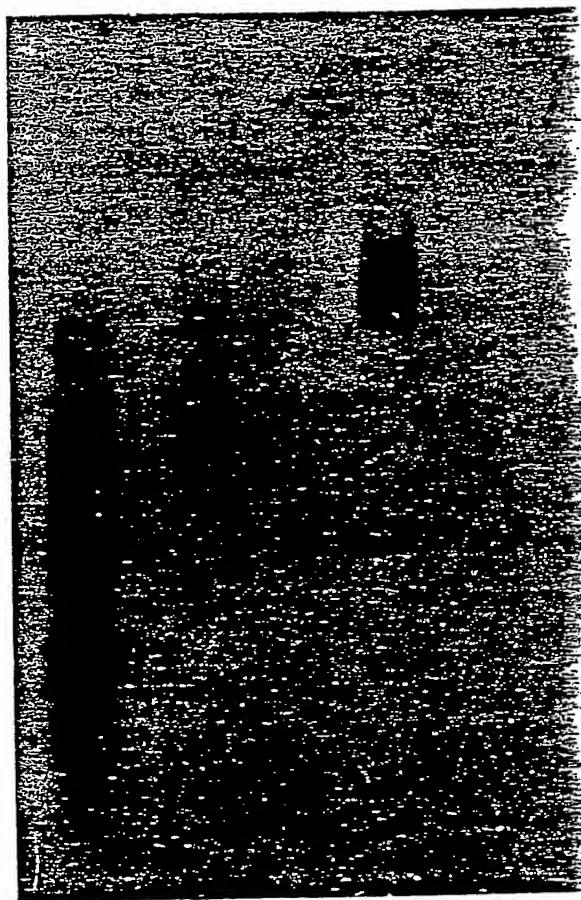


FIG. 38

48/63

1 2 3 4

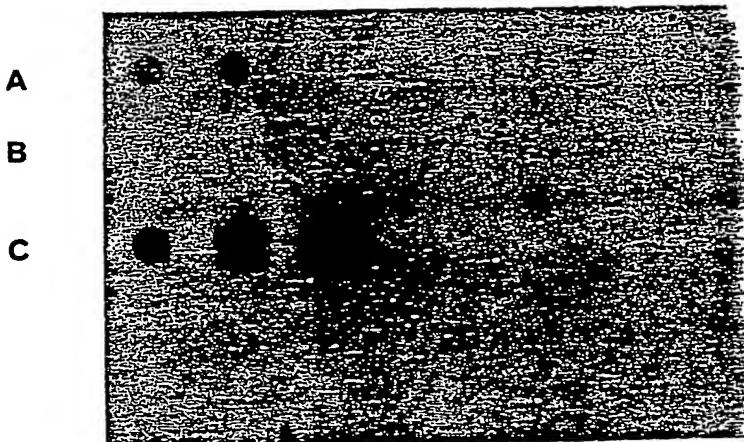


FIG. 40

A B C



FIG. 41a

I  
A B C

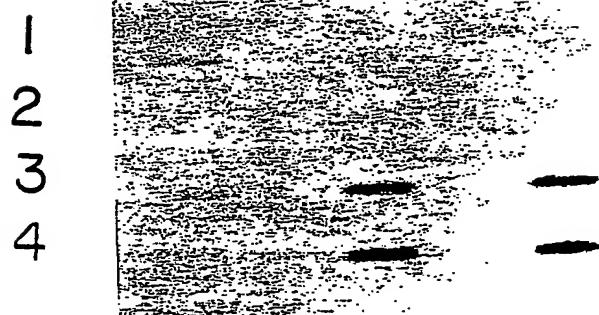


FIG. 41b

**FIG. 4I-I**

Homology between the HCV polypeptide encoded by combined ORF of clones 14i through 39c) and the non-structural protein of the Dengue flavivirus(MNWVD1).

	10	20	30	40	50	
HCV	EYVVLLFILLADARVCSC 130	LWMMLLISQAEAALEN 140	LVILNAASLAGTHGLV 150	SFLVFFCFA 160		
MNWVD1	AVSFVTLLITGNMSFRDLGRVMVMVGATMTDDIGMGV 180	TYLALLAAFKVRPTFAAGLLL 170	RKL			
HCV	60 WYLKGKWWPGAVYTFYGMW 190	70 PLLL 200	80 LALPQRAYALDTEVA 210	90 ASCGGVV 220	100 LVGLMALTL 230	
MNWVD1	TSKELMMTTIGIVLLSQSTIPETILE 240	140 LTDALALGMMVLKMVRK 250	150 MEKYQLAVT 260	160 IMAILCVP 270	110 LSPYY 280	
HCV	120 KRYISWC 180 LWWLQYFLTRVEAQLH 240 VWPPLNVRGG 300 RDAVILLMCAV 360 HPTLVDITK 420 LLAV	130 WIPPL 190 QLHV 250 LQYFL 310 TRVEA 370 QLH 430 WIPPL 490 RDAV 550 LLAV	140 EQLH 200 WIPPL 260 QLHV 320 QLH 380 RDAV 440 WIPPL 500 RDAV 560 LLAV	150 V 210 V 270 V 330 V 390 V 450 V 510 V	160 T 220 V 280 V 340 V 400 V 460 V 520 V	170 C 230 Y 290 Y 350 Y 410 Y 470 Y 530 Y
MNWVD1	TSKELMMTTIGIVLLSQSTIPETILE 240 LTDALALGMMVLKMVRK 300 MEKYQLAVT 360 IMAILCVP 420 LSPYY 480 LLAV	140 LTDALALGMMVLKMVRK 200 MEKYQLAVT 260 IMAILCVP 320 LSPYY 380 LLAV	150 MEKYQLAVT 210 IMAILCVP 270 LSPYY 330 LLAV	160 IMAILCVP 220 LSPYY 280 LLAV	110 LSPYY 170 C 230 Y 290 Y 350 Y 410 Y 470 Y 530 Y	
HCV	480 AKAVDFIPVENLETTMRSPVFTDNSSPPV 540 PGKNPRAVQT 600 AYVSAIAQTEK	490 FTDNSSPPV 550 PGTSGSPI 610 IDKKGKV 660 VGLYNGVV 720 TRSG	500 QSFQVAHL 560 GAGKTKR 620 YLP 680 AIVRGA 740 IKR	510 HAPTGSGKS 570 K	520 --TKVPAAYAAQ 580 R 640 I	530 Q 590 R 650 A 710 K 770 R
MNWVD1	540	550	560	570	580	

50/63

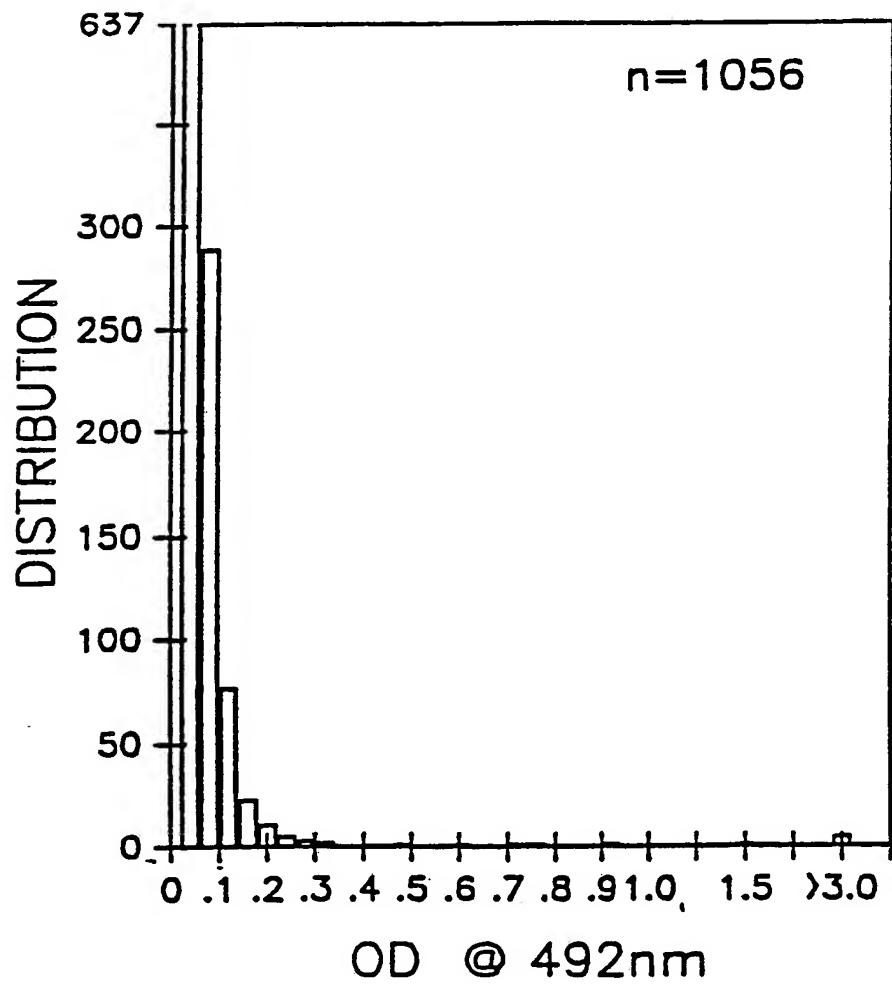
HCV	GYKVLVLNPS--VAATLGFGAYMSKAHGIDPNIRTGVRTITGGSPITYSTYGFADGGC									
MNWVD1	GLRTLILAPTRVVAEMEEALRGLPIRYQTPAIRAEHTGREIVDLMCHATFTMRLL-SPV 650 660 670 680 690 700									
HCV	590	600	610	620	630	640				
MNWVD1	SGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEV RVPNYNLIIMDEAHFTDPASIAARGYISTRVE-MGEAAGIFMTATPPGSRD-PFPQSNAF 710 720 730 740 750 760									
HCV	650	660	670	680	690	700				
MNWVD1	ALSTTGEIPFYGKAIPLEVIGGRHLIFCHSKKKCDELAALKVALGINAVAYYRGLDVSV IMDEEREIPERSWSSGHEWVTDFKGKTVWFVPSIKAGNDTAACLRKNGKKVQLSRKTFD 770 780 790 800 810 820									
HCV	710	720	730	740	750	760				
MNWVD1	IPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSRT SEYVKTRTNDWNFVVTTDISEMGANFKAERVIDPRRCMKPVILTDGEERVILAGPMPVTH 830 840 850 860 870 880									
HCV	770	780	790	800	810	820				
MNWVD1	QRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT SS									

FIG. 41-2

51/63

**FIG. 43**  
DISTRIBUTION OF RANDOM SAMPLES

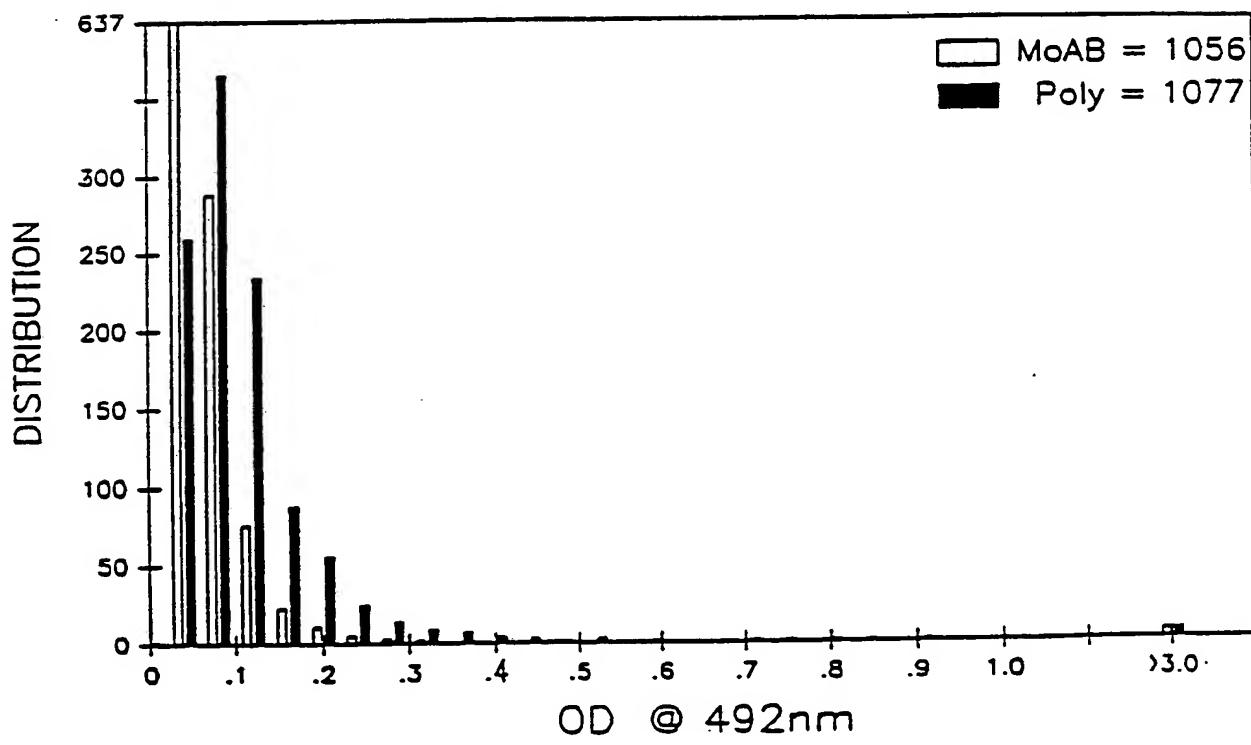
C100-3 Ag ELISA Preclinical Kit  
416ng C100/WELL, 2 HRS 37°C, 20ul SAMPLE



52/63

**FIG. 44**  
Distribution of O.D. Values for  
Random Blood Donor Samples Tested with Two ELISA  
Configurations

C100-3 Ag ELISA MoAB vs Polyclonal



**FIG. 45**

<u>Name</u>	<u>Common Sequence</u>	<u>Variable Sequence</u>
5' - 3 - 1	AAGCTTGATCGAATTTC	CGATCTTGC
- 2		CGATCCTGC
- 3		CGATCATGC
- 4		CGATCGTGC
- 5		CGAAAGTTGC
- 6		CGAAGCTGC
- 7		AGATCTTGC
- 8		AGATCCTGC
- 9		AGATCATGC
- 10		AGATCGTGC
- 11		AGAAAGTTGC
- 12		AGAAGCTGC
- 13		CGATCTTGT
- 14		CGATCCTGT
- 15		CGATCATGT
- 16		CGATCGTGT
- 17		CGAAAGTTGT
- 18		CGAAGCTGT
- 19		AGATCTTGT
- 20		AGATCCTGT
- 21		AGATCATGT
- 22		AGATCGTGT
- 23		AGAAAGTTGT
- 24		AGAAGCTGT
- 25		CGCTCTTGC
- 26		CGCTCCTGC
- 27		CGCTCATGC
- 28		CGCTCGTGC
- 29		CGCAGTTGC
- 30		CGCAGCTGC
- 31		CGCTCTTGT
- 32		CGCTCCTGT
- 33		CGCTCATGT
- 34		CGCTCGTGT
- 35		CGCAGTTGT
- 36		CGCAGCTGT

54 / 63

## FIG. 46 - | Translation of DNA k9-1

GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly  
 1 CAGGCTGTCTGAGAGGCTAGCCAGCTGCCACCCCTTACCGATTGACCAGGGCTGGG  
 GTCCGACAGGACTCTCGATCGTCGACGGCTGGGAATGGCTAAACTGGTCCCACCC

ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro  
 61 GCCCTATCAGTTATGCCAACGGAAGCGCCCCGACCAGCGCCCCACTGCTGGCACTACC  
 CGGGATAGTCAATAACGGTTGCCCTCGCCGGGCTGGTCGCGGGATGACGACCGTGATGG

ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr  
 121 CCCCAAAACCTTGCCTGCGGTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATATTGCTTCA  
 GGGGTTTGGAACGCCATAACACGGCGCTTCACACACACCAGGCCATATAACGAAGT

ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly  
 181 CTCCCAGCCCCGTGGTGGGAACGACCGACAGGTGGCGCCACCTACAGCTGGG  
 GAGGGTGGGGCACCAACACCCTTGCTGGCTGTCCAGCCCGCGGGTGGATGTCGACCC

GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe  
 241 GTGAAAATGATAACGGACGTCTCGTCTTAACAATACCAAGGCCACCGCTGGCAATTGGT  
 CACTTTACTATGCCCTGCAGAACGAGGAATTGTTATGGTCCGGTGGCGACCCGTTAACCA

GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal  
 301 TCGGTTGTACCTGGATGAACCTCAACTGGATTCAACAAAGTGTGCCAGCGCCCTCTGTG  
 AGCCAACATGGACCTACTTGAGTTGACCTAACACGCCCTGCCGGAGGAACAC

IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro  
 361 TCATCGGAGGGGGCGGGCAACAAACACCCCTGCACTGCCCACTGATTGCTTCCGCAAGCATC  
 AGTAGCCTCCCCGCCGTTGTGGACGTGACGGGTGACTAACGAAGGCCTCGTAG

AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp  
 421 CGGACGCCACATACTCTCGTGCCTCCGGCTGGATCACACCCAGGTGCCTGGTCG  
 GCCTGCCGTGTATGAGAGGCCACGCCAGGGACCTAGTGTGGGTCCACGGACCAAGC

---

TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg  
 481 ACTACCCGTATAGGCTTGGCATTATCCTGTACCATCAACTACACTATATTAAAATCA  
 TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGATATAAAATTAGT

---

MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu  
 541 GGATGTACGTGGGAGGGGTCGAGCACAGGCTGGAAGCTGCCACTGGACGCCGGCG  
 CCTACATGCACCCCTCCCCAGCTCGTCCGACCTTCGACGGACGTTGACCTGCGCCCCGC

---

ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr  
 601 AACGTTGCGATCTGGAAGATAGGGACAGGTCCGAGCTCAGCCGTTACTGCTGACCAACTA  
 TTGCAACGCTAGACCTCTATCCCTGTCCAGGCTCGAGTCGGCAATGACGACTGGTGAT

---

GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle  
 661 CACAGTGGCAGGTCTCCCCTGTTCTCACAAACCCCTGCCAGCCTGTCCACCGGCCTCA  
 GTGTCACCGTCCAGGAGGGACAAGGAAGTGTGGACGGTCGGAACAGGTGGCCGGAGT

-----Overlap with Combined ORF of DNAs 12f through 15e-----  
 HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla  
 721 TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGTCAAGCATCG  
 AGGTGGAGGTGGTCTTGTAAACACCTGCACGTATGAAACATGCCCAACCCAGTTCGTAGC

---

SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuAlaAspAlaArg  
 781 CGTCCTGGGCCATTAAGTGGAGTACGTCGTCCTCTGTTCTGCTTCAGACGCCGCG  
 GCAGGACCCGGTAATTCACCTCATGCAGCAGGAGGACAAGGAAGACGAACGTCTGCCGCG

55/63

841 ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn  
 GCGTCTGCTCCTGCTTGATGATGCTACTCATATCCCAAGCGGAAGCGGCTTGAGA  
 CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTGCCCTCGCCGAAACCTCT

---

901 LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal  
 ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGACGCACGGTCTGTATCCTTCCTCG  
 TGGAGCATTATGAATTACGTCGTAGGGACCAGGGCTGCCAGAACATAGGAAGGAGC

---

961 PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPhe  
 TGTTCTCTGCTTGCATGGTATCTGAAGGGTAAGTGGGTGCCCGAGCGGTCTACACCT  
 ACAAGAACGAAACGTACCATAGACTCCCATTACCCACGGGCCTGCCAGATGTGGA

---

1021 TyrGlyMetTrpProLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeu  
 TCTACGGGATGTGGCCTCTCCTGCTCTGTTGGCGTGTGCCCCAGCGGGCGTACGCGC  
 AGATGCCCTACACCGGAGAGGAGGACGAGGACAACCGCAACGGGGTCGCCCGATGCGCG

---

1081 AspThrGluValAlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThr  
 TGGACACGGAGGTGGCCGCGTCGTGTCGGTGTGTTCTCGTGGTTGATGGCGCTAA  
 ACCTGTGCCCTCCACCGCGCAGCACACGCCAACAAAGAGCAGCCAACTACCGCGATT

---

1141 LeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeu  
 CTCTGTCACCATATTACAAGCGCTATATCAGCTGGTGTGTTGGCTTCAGTATTTC  
 GAGACAGTGGTATAATGTCGCGATATAGTCGACCAACACCACCGAAGTCATAAAAG

---

1201 ThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArg  
 TGACCAGAGTGGAAAGCGCAACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGC  
 ACTGGTCTCACCTCGCGTTGACGTGACACCTAACGGGGGGAGTTGCAGGGCTCCCCCG

---

1261 AspAlaValIleLeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLys  
 GCGACGCTGTCATCTTACTCATGTGTGCTGTACACCCGACTCTGGTATTGACATCACCA  
 CGCTGCGACAGTAGAATGAGTACACACGACATGTGGGCTGAGACCATAACTGTAGTGGT

---

1321 LeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAla  
 AATTGCTGCTGGCCGTCTCGGACCCCTTGAGATTCTCAAGCCAG  
 TTAACGACGACCGGCAGAACCTAACGAAAGTTCGGT

FIG. 46-2

56/63

## FIG. 47-1 COMBINED ORF OF DNAs K9-1 through 15e

1 GlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGlyTrpGly  
 1 CAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTGACCAGGGCTGGG  
 GTCCGACAGGACTCTCGATCGGTGACGGCTGGGAATGGCTAAACTGGTCCCACCC  
  
 61 ProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrPro  
 61 GCCCTATCAGTTATGCCAACGGAAGCGGCCCGACCAGCGCCCTACTGCTGGCACTACC  
 CGGGATAGTCAATACGGTTGCCTTCGCCGGGCTGGTCGCGGGGATGACGACCGTGATGG  
  
 121 ProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCysPheThr  
 121 CCCCAAACCTTGCCTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATAATTGCTTC  
 GGGGTTTGGAACGCCATAACACACGGCGCTTCTCACACACACCAGGCCATATAACGAAGT  
  
 181 ProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSerTrpGly  
 181 CTCCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTGGGCCGCCACCTACAGCTGGG  
 GAGGGTCGGGCAACCACCACCTGCTGGTCCAGCCCCGCGCGGGTGGATGTCGACCC  
  
 241 GluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsnTrpPhe  
 241 GTGAAAATGATACTGGACGTCTCGCTTAACAATACCAAGGCCACCGCTGGCAATTGGT  
 CACTTTACTATGCCTGAGAACAGCAGGAATTGTATGGTCCGGTGGCGACCCGTTAACCA  
  
 301 GlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCysVal  
 301 TCGGTTGTACCTGGATGAACACTGGATTCAACAAAGTGTGGAGGCCCTCCTTGTG  
 AGCACAACATGGACCTACTTGAGTTGACCTAAGTGGTTCACACGCCCTCGCGGAGGAACAC  
  
 361 IleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisPro  
 361 TCATCGGAGGGCCGGCAACAACACCCCTGCACTGCCCACTGATTGCTCCGCAAGCATC  
 AGTAGCCTCCCCGCCGTGTTGACGTGACGGGTGACTAACGAAGGCCTCGTAG  
  
 421 AspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeuValAsp  
 421 CGGACGCCACATACTCTCGGTGCCCTGGATCACACCCAGGTGCCTGGTCG  
 GCCTGCGGTGTATGAGAGGCCACGCCAGGGACCTAGTGTGGTCCACGGACCAGC  
  
 481 TyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLysIleArg  
 481 ACTACCCGTATAGGCTTGGCATTATCCTGTACCATCAACTACACCATAATTAAAATCA  
 TGATGGGCATATCCGAAACCGTAATAGGAACATGGTAGTTGATGTGGTATAAATTAGT  
  
 541 MetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArgGlyGlu  
 541 GGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCACACTGGACGCCGGCG  
 CCTACATGCACCCCTCCCCAGCTTGTGTCGACGGACGTTGACCTGCGCCCCCGC  
  
 601 ArgCysAspLeuGluAspArgAspArgSerGluLeuSerProLeuLeuLeuThrThrThr  
 601 AACGTTGCGATCTGGAAAGACAGGGACAGGTCCGAGCTCAGCCCGTTACTGCTGACCACTA  
 TTGCAACGCTAGACCTTCTGTCCTGTCCAGGCTCGAGTCGGCAATGACGACTGGTGAT  
  
 661 GlnTrpGlnValLeuProCysSerPheThrThrLeuProAlaLeuSerThrGlyLeuIle  
 661 CACAGTGGCAGGTCTCCGTGTTCTTCACAACCCCTACCAGCCTTGTCCACCGGCTCA  
 GTGTCAACCGTCCAGGAGGGACAAGGAAGTGTGGATGGTCGGAACAGGTGGCCGGAGT  
  
 721 HisLeuHisGlnAsnIleValAspValGlnTyrLeuTyrGlyValGlySerSerIleAla  
 721 TCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGTCAAGCATCG  
 AGGTGGAGGTGGTCTTGTAAACACCTGCACGTCAATGCCCCACCCAGTTCTGAGC  
  
 781 SerTrpAlaIleLysTrpGluTyrValValLeuLeuPheLeuLeuAlaAspAlaArg  
 781 CGTCCCTGGGCCATTAAAGTGGGAGTACGTCGTTCTCCTGTGCTTGAGACGC  
 GCAGGACCCGGTAATTACCCCTCATGCAGCAAGAGGACAAGGAAGACGAACGTCTGCGCG  
  
 841 ValCysSerCysLeuTrpMetMetLeuLeuIleSerGlnAlaGluAlaAlaLeuGluAsn  
 841 GCGTCTGCTCTGCTTGTGGATGATGCTACTCATATCCAAGCGGAGGGCTTGGAGA  
 CGCAGACGAGGACGAACACCTACTACGATGAGTATAGGGTTCGCCCTCCGCCAACCTCT  
  
 901 LeuValIleLeuAsnAlaAlaSerLeuAlaGlyThrHisGlyLeuValSerPheLeuVal  
 901 ACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTATCCTTCCTCG  
 TGGAGCATTATGAATTACGTCGTAGGGACCGGCCCTGCGTGCAGAACATAGGAAGGAGC

57/63

PhePheCysPheAlaTrpTyrLeuLysGlyLysTrpValProGlyAlaValTyrThrPhe  
 961 TGGTCTTCTGCTTGCATGGTATTGAAGGGTAAGTGGGTGCCCGGAGCGGTCTACACCT  
 ACAAGAAGACGAAACGTACCATAACTCCCATTCACCCACGGGCCTGCCAGATGTGGA

TyrGlyMetTrpProLeuLeuLeuLeuLeuAlaLeuProGlnArgAlaTyrAlaLeu  
 1021 TCTACGGGATGTGGCCTCTCCTCCTGCTCCTGTGGCGTTGCCAGCGGGGTACGCGC  
 AGATGCCCTACACCAGAGGAGGACGAGGACAACCGCAACGGGTCGCCATGCGCG

AspThrGluValAlaAlaSerCysGlyGlyValValLeuValGlyLeuMetAlaLeuThr  
 1081 TGGACACGGAGGTGGCCCGCGTGTGGCGGTGTTCTCGTCGGGTTGATGGCGCTGA  
 ACCTGTGCCTCCACCAGCGCACACCGCCACAACAAGAGCAGCCAACCGCAGACT

LeuSerProTyrTyrLysArgTyrIleSerTrpCysLeuTrpTrpLeuGlnTyrPheLeu  
 1141 CTCTGTCACCATAATTACAAGCGCTATATCAGCTGGTGGCTGTTGAGTATTTC  
 GAGACAGTGGTATAATGTTCGCGATATAGTCGACCAACGAAACACCACCGAAGTCATAAAAG

ThrArgValGluAlaGlnLeuHisValTrpIleProProLeuAsnValArgGlyGlyArg  
 1201 TGACCAGAGTGGAAAGCGCAACTGCACGTGTGGATTCCCCCTCAACGTCCGAGGGGGGC  
 ACTGGTCTCACCTCGCGTTGACGTGACACCTAACGGGGAGTTGCAGGCTCCCCCG

AspAlaValIleLeuLeuMetCysAlaValHisProThrLeuValPheAspIleThrLys  
 1261 GCGACGCCGTATCTTACTCATGTGTGCTGTACACCGACTCTGGTATTGACATCACCA  
 CGCTGCGCAGTAGAACATGAGTACACACGACATGTGGGCTGAGACCATAACTGTAGTGGT

LeuLeuLeuAlaValPheGlyProLeuTrpIleLeuGlnAlaSerLeuLeuLysValPro  
 1321 AATTGCTGCTGGCCGTCTCGGACCCCTTGGATTCTCAAGCCAGTTGCTTAAAGTAC  
 TTAACGACGACCGGAGAACCTAACAGAACGCGTAAAGAACGCGCTAACGAATTTCATG

TyrPheValArgValGlnGlyLeuLeuArgPheCysAlaLeuAlaArgLysMetIleGly  
 1381 CCTACTTTGTGCGCGTCCAAGGCCTTCTCCGGTCTGCGCGTTAGCGCGGAAGATGATCG  
 GGATGAAACACGCGCAGGTTCCGGAAGAGGCCAACGCGCAATCGGCCTTACTAGC

GlyHisTyrValGlnMetValIleIleLysLeuGlyAlaLeuThrGlyThrTyrValTyr  
 1441 GAGGCCATTACGTGCAAATGGTCATCATTAAGTTAGGGCGCTTACTGGCACCTATGTT  
 CTCCGGTAATGCACGTTACCAGTAGTAATTCAATCCCCCGAATGACCCTGGATACAAA

AsnHisLeuThrProLeuArgAspTrpAlaHisAsnGlyLeuArgAspLeuAlaValAla  
 1501 ATAACCATCTCACTCCTCTCGGACTGGCGCACACGGCTTGCGAGATCTGGCGTGG  
 TATTGGTAGAGTGAGGAGAACGCGTGGCCGACGCTAGACCGGGCACC

ValGluProValValPheSerGlnMetGluThrLysLeuIleThrTrpGlyAlaAspThr  
 1561 CTGTAGAGCCAGTCGTCTCTCCAAATGGAGACCAAGCTCATCACGTGGGGGGCAGATA  
 GACATCTCGGTCAAGCAGAACAGAGGGTTACCTCTGGTCAGTAGTGCACCCCCCGTCTAT

AlaAlaCysGlyAspIleIleAsnGlyLeuProValSerAlaArgArgGlyArgGluIle  
 1621 CCGCCCGCGTGCAGCATCATCAACGGCTTGCGCTGTTCCGCCAGGGGGCGGGAGA  
 GGCAGCGCACGCCACTGTAGTAGTTGCCGAACGGACAAAGCGGGCGTCCCCGCCCTCT

LeuLeuGlyProAlaAspGlyMetValSerLysGlyTrpArgLeuLeuAlaProIleThr  
 1681 TACTGCTCGGGCCAGCCGATGGAATGGCTCCAAGGGGTGGAGGTGCTGGCGCCCATCA  
 ATGACGAGCCCAGCTGGCTACCTTACCAAGAGGTCCCCACCTAACGACCGCGGGTAGT

AlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysIleIleThrSerLeuThrGlyArg  
 1741 CGCGTACGCCAGCAGACAAGGGGCCCTCTAGGGTGCATAATCACCAGCCTAACTGGCC  
 GCCGCATGCCGGTGTGTTCCCCGGAGGATCCCACGTATTAGTGGTGGATTGACCGGG

AspLysAsnGlnValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeu  
 1801 GGGACAAAAACCAAGTGGAGGGTGAGGTCCAGATTGTGTCACGTGCTGCCAAACCTCC  
 CCCTGTTGGTACCTCCACTCCAGGTCTAACACAGTTGACGACGGGTTGGAAAGG

AlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAlaGlyThrArgThrIle  
 1861 TGGCAACGTGCATCAATGGGGTGTGGACTGTCTACACGGGGCCGGAACGAGGACCA  
 ACCGTTGCACGTAGTTACCCACACGACCTGACAGATGGTGCCTGGCTCGTCTGGT

AlaSerProLysGlyProValIleGlnMetTyrThrAsnValAspGlnAspLeuValGly

FIG. 47-2

SUBSTITUTE SHEET

58/63

1921 TCGCGTCACCCAAGGGTCTGTCATCCAGATGTATACCAATGTAGACCAAGAACCTTGTGG  
 AGCGCAGTGGTTCCCAGGACAGTAGGTCTACATATGGTTACATCTGGTTCTGGAACACC  
 TrpProAlaProGlnGlySerArgSerLeuThrProCysThrCysGlySerSerAspLeu  
 1981 GCTGGCCCGCTCCGCAAGGTAGCCGCTCATTGACACCCCTGCACTTGC GGCTCCTCGGAC  
 CGACCGGGCGAGGCCTCCATCGGCGAGTAACGTGGGACGTAAACGCCGAGGAGCCTGG  
 TyrLeuValThrArgHisAlaAspValIleProValArgArgGlyAspSerArgGly  
 2041 TTTACCTGGTCACGAGGCACGCCGATGTCATTCCCGTGC GCCGGGGTGATAGCAGGG  
 AAATGGACCACTGCTCCGTGCGGCTACAGTAAGGCACGCCGGCCCCACTATCGTCCC  
 SerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSerGlyGlyProLeuLeu  
 2101 GCAGCCCTGCTGTCGCCCGGCCATTCCCTACTTGAAAGGCTCCTCGGGGGTCCGCTGT  
 CGTCGGACGACAGCGGGCCGGTAAAGGATGAACCTTCCGAGGAGCCCCCAGGCGACA  
 CysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCysThrArgGlyValAla  
 2161 TGTGCCCGCGGGGCACGCCGTGGCATATTAGGGCCGCGTGTGCACCCGTGGAGTGG  
 ACACGGGGCGCCCGTGC GGCACCCGTATAAATCCGGC GACACGTGGGACCTCAC  
 LysAlaValAspPheIleProValGluAsnLeuGluThrThrMetArgSerProValPhe  
 2221 CTAAGGCGGTGGACTTTATCCCTGTGGAGAACCTAGAGACAAACCATGAGGTCCCCGGTGT  
 GATTCCGCCACCTGAAATAGGGACACCTCTGGATCTCTGTGGTACTCCAGGGGCCACA  
 ThrAspAsnSerSerProProValValProGlnSerPheGlnValAlaHisLeuHisAla  
 2281 TCACGGATAACTCCTCTCACCAGTAGTGGCTCAGGCTCACCTCCATG  
 AGTGCCTATTGAGGAGAGGTGGTCATCACGGGTCTCGAAGGTCCACCGAGTGGAGGTAC  
 ProThrGlySerGlyLysSerThrLysValProAlaAlaTyrAlaAlaGlnGlyTyrLys  
 2341 CTCCCCACAGGCAGCGGAAAAGCACCAAGGTCCC GGCTGCATATGCAGCTCAGGGCTATA  
 GAGGGTGTCCCGTCCGGTTTCGTGGTCCAGGGCCACGTATACTCGAGTCCCAGTAT  
 ValLeuValLeuAsnProSerValAlaAlaTyrLeuGlyPheGlyAlaTyrMetSerLys  
 2401 AGGTGCTAGTACTCAACCCCTCTGTTGCTGAAACACTGGGTTGGCTTACATGTCCA  
 TCCACGATCATGAGTTGGGAGACAACGACGTTGTGACCCGAAACACGAATGTACAGGT  
 AlaHisGlyIleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerPro  
 2461 AGGCTCATGGGATCGATCTAACATCAGGACCGGGGTGAGAACAAATTACCAACTGGCAGCC  
 TCCGAGTACCCCTAGCTAGGATTGTAGTCCTGGCCCCACTCTGTTAACGGTGACCGTCGG  
 IleThrTyrSerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyAlaTyr  
 2521 CCATCACGTACTCCACCTACGGCAAGTCCCTGCCGACGGCGGGTGCTCGGGGGCGCTT  
 GGTAGTGCATGAGGTGGATGCCGTTCAAGAACGGCTGCCACAGGCCCCCGCGAA  
 AspIleIleIleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGly  
 2581 ATGACATAATAATTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTGGGCATCG  
 TACTGTATTATTAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAGC  
 ThrValLeuAspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaTyrAlaTyr  
 2641 GCACTGTCCTTGACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCA  
 CGTGACAGGAACGGTTCGTCTGACGCCCGCTCTGACCAACACGAGCGGTGGCGGT  
 ProProGlySerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThr  
 2701 CCCCTCCGGGCTCCGTCACTGTGCCCATCCAAACATCGAGGAGGTGCTCTGTCCACCA  
 GGGGAGGCCCCGAGGCAGTGACACGGGTAGGGTTGTAGTCCTCCAAACGAGACAGGTGGT  
 GlyGluIleProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHis  
 2761 CCGGAGAGATCCCTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGAGAC  
 GGCCTCTCTAGGGAAAAATGCCGTTCCGATAGGGGAGCTTCATTAGTCCCCCCCCTCTG  
 LeuIlePheCysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeu  
 2821 ATCTCATCTTCTGTCATTCAAAGAAGAAGTGCACGAACTCGCCGAAAGCTGGTCGCAT  
 TAGAGTAGAACAGTAAGTTCTTCTTCACGCTGCTTGA GCGCTTCTGACCGAGCGTA  
 GlyIleAsnAlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGly  
 2881 TGGGCATCAATGCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCG  
 ACCCGTAGTTACGGCACCGGATGATGGCGCAGAACACTGCACAGGCAGTAGGGCTGGTCGC

59/63

AspValValValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSer  
 2941 GCGATGTTGTCGTGGCAACCGATGCCCTCATGACC GGCTATACCGGCAGACTTCGACT  
 CGCTACAACAGCAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGA

ValIleAspCysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPhe  
 3001 CGGTGATAGACTGCAAATACGTGTCAACCAGACAGTCGATTCAGCCTTGACCCCTACCT  
 GCCACTATCTGACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGA

ThrIleGluThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArg  
 3061 TCACCATTGAGACAATCACGCTCCCCCAGGATGCTGTCTCCGCACTAACGTCGGGGCA  
 AGTGGTAACTCTGTTAGTGCAGGGGGCCTACGACAGAGGGCGTAGTTGCAGCCCCGT

ThrGlyArgGlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGly  
 3121 GGACTGGCAGGGGGAAAGCCAGGCATCTACAGATTTGTCGGCACCGGGGGAGCGCCCTCCG  
 CCTGACCGTCCCCCTCGGTCCGTAGATGTCTAACACACC GTGGCCCCCTCGCGGGGAGGC

MetPheAspSerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeu  
 3181 GCATGTTCGACTCGTCCGTCCCTGTGAGTGCTATGACGCAGGCTGTGCTTGATGAGC  
 CGTACAAGCTGAGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCG

ThrProAlaGluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProVal  
 3241 TCACGCCCGCCGAGACTACAGTTAGGCTACGAGCGTACATGAACACCCGGGGCTCCCG  
 AGTGCGGGCGGCTCTGATGTCAATCCGATGCTCGATGTACTTGTGGGGCCCCGAAGGGC

CysGlnAspHisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAla  
 3301 TGTGCCAGGACCATCTGAATTGGGAGGGCGCTTTACAGGCCTCACTCATATAGATG  
 ACACGGTCCTGGTAGAACTTAAACCCCTCCGCAGAAATGTCCGGAGTGAGTATATCTAC

HisPheLeuSerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGln  
 3361 CCCACTTCTATCCCAGACAAAGCAGAGTGGGGAGAACCTCCTTACACTGGTAGCGTACC  
 GGGTGAAAGATAGGGCTGTCTCGTCTACCCCTCTGGAAAGGAATGGACCATCGCATGG

AlaThrValCysAlaArgAlaGlnAlaProProSerTrpAspGlnMetTrpLysCys  
 3421 AAGCCACCGTGTGCGCTAGGGCTCAAGCCCTCCCCATCGTGGGACCAGATGTGGAAAGT  
 TTCGGTGGCACACCGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCCTGGTCTACACCTCA

LeuIleArgLeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAla  
 3481 GTTGATTGCCCTCAAGCCCACCCCTCCATGGGCCAACACCCCTGCTATACAGACTGGCG  
 CAAACTAAGCGGAGTTCGGGTGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGC

ValGlnAsnGluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSer  
 3541 CTGTTCAAGGAAATCACCTGACGCACCCAGTCACCAATAACATCATGACATGCATGT  
 GACAAGTCTTACTTAGTGGACTGCGTGGTCAGTGGTTATGTAGTACTGTACGTACA

AlaAspLeuGluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeu  
 3601 CGGCCGACCTGGAGGTGCGTACAGCACCTGGGTGCTCGTGGCGCGTCTGGCTGCTT  
 GCCGGCTGGACCTCCAGCAGTGCCTGGACCCACGAGCAACGCCAGGACCGACGAA

AlaAlaTyrCysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGly  
 3661 TGGCCCGTATTGCCGTCAACAGGCTGCGTGGTCATAGTGGGAGGGCTGCTTGTCCG  
 ACCGGCGATAACGGACAGTTGTCGACGCACCAGTACCCGTCCAGCAGAACAGGC

LysProAlaIleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGlu  
 3721 GGAAGCCGCGAACATCACCTGACAGGGAACTCCTACCGAGAGTTCGATGAGATGGAAG  
 CCTTCGGCCGTTAGTATGGACTGTCCTCAGGAGATGGCTCTCAAGCTACTCACCTTC

CysSerGlnHisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGln  
 3781 AGTGCTCTCAGCACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGC  
 TCACGAGAGTCGTGAATGGCATGTAGCTCGTCCCTACTACGAGCGCTCGTCAAGTTCG

LysAlaLeuGlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaVal  
 3841 AGAAGGCCCTGGCCTCCTGCGAGACC CGCGTCCCGTCAGGAGAGGTATGCCCTGCTG  
 TCTTCCGGGAGCCGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGAC

GlnThrAsnTrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSer

FIG. 47-4

SUBSTITUTE SHEET

60/63

3901 TCCAGACCAACTGGCAAAACTCGAGACCTCTGGCGAAGCATATGTGGAACTTCATCA  
AGGTCTGGT1GACCGTTTGAGCTCTGGAAAGACCCGCTCGTATACACCTGAAGTAGT

GlyIleGlnTyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeu  
3961 GTGGGATAACAATACTTGGCGGGCTGTCAACGCTGCCTGGTAACCCGCCATTGCTTCAT  
CACCTATGTTATGAACCGCCGAACAGTTGCGACGGACCATTGGGGCGGTAAACGAAGTA

MetAlaPheThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsn  
4021 TGATGGCTTTACAGCTGCTGTCACCAGCCCCTAACCAACTAGCCAAACCTCCTCTCA  
ACTACCGAAAATGTCGACGACAGTGGTCGGGTGATTGGTGATCGTTGGGAGGAGAAGT

IleLeuGlyGlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheVal  
4081 ACATATTGGGGGGGTGGGTGGCTGCCAGCTGCCGCCGGTGCCGCTACTGCCTTG  
TGTATAACCCCCCCCACCCACCGACGGGTCGAGCGGGCGGGCCACGGCGATGACGGAAAC

GlyAlaGlyLeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAsp  
4141 TGGGCGCTGGCTAGCTGGCGCCATCGGAGTGGACTGGGAAGGTCCTCATAG  
ACCCCGCACCGAACATCGACCGCGGGTAGCCGTACAACCTGACCCCTCAGGAGTATC

IleLeuAlaGlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSer  
4201 ACATCCTTGCAAGGGTATGGCGCGGGGTGGCTCTTGTCATTCAAGATCATGA  
TGTAGGAACGTCCCATAACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACT

GlyGluValProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGly  
4261 GCGGTGAGGTCCCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTGCCCG  
CGCCACTCCAGGGAGGTGCCCTCTGGACCAAGTTAGATGACGGCGGTAGGAGAGCGGGC

AlaLeuValValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGlu  
4321 GAGCCCTCGTAGTCGGCGTGGCTGTGCAGCAACTGCGCCGGCACGTTGGCCCGGGCG  
CTCGGGAGCATCAGCCGACCAAGAACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGC

GlyAlaValGlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSer  
4381 AGGGGGCAGTGCAGTGGATGAACCGGCTGATAGCCTCGCCTCCGGGGAAACATGTT  
TCCCCCGTCACGTACCTACTTGGCGACTATCGGAAGCGGAGGGCCCCCTGGTACAAA

ProThrHisTyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSer  
4441 CCCCCACGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCA  
GGGGGTGCGTGATGCACGCCCTCGCTACGTCACGGCGCAGTGACGGTATGAGTCGT

LeuThrValThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThr  
4501 GCCTCACTGTAACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTGGAGTGTACCA  
CGGAGTGACATTGGTCGAGGACTCCGCTGACGTGGTCACCTATTGAGCCTCACATGGT

ProCysSerGlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAsp  
4561 CTCCATGCTCCGGTTCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCG  
GAGGTACGAGGCCAAGGACCGATTCCCTGTAGACCCCTGACCTATACGCTCCACAACCGC

PheLysThrTrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSer  
4621 ACTTTAACGACTGGCTAAAGCTAACGCTCATGCCACAGCTGCCCTGGATCCCTTGTGT  
TGAAATTCTGGACCGATTTCGATTGAGTACGGTGTGACGGACCCCTAGGGGAAACACA

CysGlnArgGlyTyrLysGlyValTrpArgValAspGlyIleMetHisThrArgCysHis  
4681 CCTGCCAGCGCGGGTATAAGGGGGTCTGGCGAGTGGACGGCATATGCACACTCGCTGCC  
GGACGGTCGCGCCCATATTCCCCCAGACCGCTCACCTGCCGTAGTACGTGTGAGCGACGG

CysGlyAlaGluIleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArg  
4741 ACTGTGGAGCTGAGATCACTGGACATGTCAAAACGGGACGATGAGGATCGTCGGTCCTA  
TGACACCTCGACTCTAGTACCTGTACAGTTTGCCCTGCTACTCCTAGCAGCCAGGAT

ThrCysArgAsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCys  
4801 GGACCTGCAAGAACATGTGGAGTGGACCTTCCCCATAATGCCCTACACCACGGGCCCT  
CCTGGACGTCCTGTACACCTCACCTGGAAAGGGGTAATTACGGATGTGGTGCCCGGGGA

ThrProLeuProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyr  
4861 GTACCCCCCTCTGCGCGAACATACACGTTGCGCTATGGAGGGTGTGAGAGGAAT  
CATGGGGGAAGGACGCGCGTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTA

FIG. 47-5

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61/63

ValGluIleArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeu  
 4921 ATGTGGAGATAAGGCAGGTGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATC  
 TACACCTCTATTCCGCCACCCCCCTGAAGGTGATGCACTGCCATACTGATGACTGTTAG

LysCysProCysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeu  
 4981 TCAAATGCCGTGCCAGGTCCCATGCCGAATTTTACAGAATTGGACGGGGTGC  
 AGTTTACGGGACGGTCCAGGGTAGCGGGCTAAAAAGTGTCTAACCTGCCACGCGG

HisArgPheAlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGly  
 5041 TACATAGGTTTGCCTCCCTGCAAGCCCTTGCTGCGGGAGGTATCATTAGAGTAG  
 ATGTATCCAAACGCCGGGGACGTTAGCGTTAACGACGCCCTCCATAGTAAGTCTCATC

LeuHisGluTyrProValGlySerGlnLeuProCysGluProGluProAspValAlaVal  
 5101 GACTCCACGAATACCCGGTAGGGTCGCAATTACCTTGCGAGCCGAACCGGACGTGGCG  
 CTGAAGGTGCTTATGGGCCATCCCAGCGTTAACGACGCTCGGGCTGGCCTGCACCAGG

LeuThrSerMetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeu  
 5161 TGTTGACGTCCATGCTCACTGATCCCTCCATATAACAGCAGAGGCGGCCGGCGAAGGGT  
 ACAACTGCAGGTACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCGCTTCCA

AlaArgGlySerProProSerValAlaSerSerAlaSerGlnLeuSerAlaProSer  
 5221 TGGCGAGGGGATCACCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCAT  
 ACCGCTCCCTAGTGGGGGAGACACCAGGTCGAGGAGGCCATCGGTGATAGGCGAGGTA

LeuLysAlaThrCysThrAlaAsnHisAspSerProAspAlaGluIleGluAlaAsn  
 5281 CTCTCAAGGCAACTTGCACCGCTAACCATGACTCCCTGATGCTGAGCTCATAGAGGCCA  
 GAGAGTTCCGTTAACGTTGGCGATTGGTACTGAGGGACTACGACTCGAGTATCTCCGGT

LeuLeuTrpArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysVal  
 5341 ACCTCCTATGGAGGCAGGAGATGGGCGGAAACATCACCAGGGTTGAGTCAGAAAACAAAG  
 TGGAGGATACTCCGCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTGTTC

ValIleLeuAspSerPheAspProLeuValAlaGluGluAspGluArgGluIleSerVal  
 5401 TGGTGATTCTGGACTCCTTCGATCCGCTTGTGGCGGAGGAGCAGCAGGAGATCTCCG  
 ACCACTAACGACCTGAGGAAGCTAGGCGAACACCCGCCCTCTGCTCGCCCTAGAGGC

ProAlaGluIleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArg  
 5461 TACCCGAGAAATCTGCGGAAGTCTCGGAGATTGCCCTGCCGTTGGCGC  
 ATGGGCGTCTTAGGACGCCCTCAGAGCCTCTAACGGGTCGGGACGGGAAACCCGGCG

ProAspTyrAsnProProLeuValGluThrTrpLysProAspTyrGluProProVal  
 5521 GCCCGGACTATAACCCCCCGCTAGTGGAGACGTGGAAAAGCCGACTACGAACCACCTG  
 CCGGCCTGATATTGGGGGGCGATCACCTCTGCACCTTTGCCGTTGCTGGTGGAC

ValHisGlyCysProLeuProProLysSerProProValProProArgLysLys  
 5581 TGGTCCATGGCTGCGCTTCCACCTCCAAAGTCCCTCTGTGCCCTCGCCTCGGAAGA  
 ACCAGGTACCGACAGGGCAAGGTGGAGGTTCAAGGGAGGACACGGAGGCGAGCCTCT

ArgThrValValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArg  
 5641 AGCGGACGGTGGCTCCTACTGAATCACCTATCTACTGCGCTGGCCGAGCTCGCCACCA  
 TCGCCTGCCACCAGGAGTGACTTAGTGGGATAGATGACGGAACCGGCTCGAGCGGTGGT

SerPheGlySerSerSerThrSerGlyIleThrGlyAspAsnThrThrSerSerGlu  
 5701 GAAGCTTGGCAGCTCCTCAACTCCGGCATTACGGGCGACAATACGACAACATCCTCTG  
 CTCGAAACCGTCGAGGAGTTGAAGGCCGTAATGCCGCTGTTATGCTGTTAGGAGAC

ProAlaProSerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProPro  
 5761 AGCCCGCCCTCTGGCTGCCCGACTCCGACGCTGAGTCCTATTCCCTCCATGCCCG  
 TCGGGCGGGGAAGACCGACGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGG

LeuGluGlyGluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSer  
 5821 CCCTGGAGGGGGAGCTGGGATCCGGATCTAGCGACGGGTATGGTCAACGGTCAGTA  
 GGGACCTCCCCCTCGGACCCCTAGGCCTAGAACGCTGCCCAGTACCAAGTTGCCAGTCAT

GluAlaAsnAlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeu

FIG. 47-6

SUBSTITUTE SHEET

62/63

5881 GTGAGGCCAACCGCGGAGGATGTCGTGCTGCCTCAATGCTTACTCTGGACAGGCGCAC  
CACTCCGGTTGCGCCTCCTACAGCACAGCAGTTACAGAATGAGAACCTGTCCCGCTG  
ValThrProCysAlaAlaGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeu  
5941 TCGTCACCCCCGTGCGCGGAAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGT  
AGCAGTGGGGCACGGCGCCTTCTGTCTTGACGGTAGTTACGTGATTGTTGAGCA  
LeuArgHisHisAsnLeuValTyrSerThrSerArgSerAlaCysGlnArgGlnLys  
6001 TGCTACGTCACCACAATTGGTGTATTCCACCACCTCACGAGTGCTGCCAAAGGCAGA  
ACGATGCACTGGTGTAAACACATAAGGTGGAGTGCACGAACGGTTCCGTCT  
LysValThrPheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGlu  
6061 AGAAAAGTCACATTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGG  
TCTTCAGTGTAAACTGTCTGACGTTCAAGACCTGTCGTAATGGTCTGCATGAGTTCC  
ValLysAlaAlaAlaSerLysAlaAsnLeuLeuSerValGluGluAlaCysSer  
6121 AGGTTAAAGCAGCGCGTAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCA  
TCCAATTGTCGCCGCAGTTCACTCCGATTGAACGATAGGCATCTCCTCGAACGT  
LeuThrProProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCys  
6181 GCCTGACGCCCCCACACTCAGCAAATCCAAGTTGGTATGGGCAAAAGACGTCCGTT  
CGGACTGCGGGGGTGTGAGTCGGTTAGGTTCAAACCAATACCCGTTTCTGCAGGCAA  
HisAlaArgLysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAsn  
6241 GCCATGCAAGAAAGGCCGTAACCCACATCAACTCCGTGGAAAGACCTCTGGAAAGACA  
CGGTACGGTCTTCCGGATTGGGTGAGTGGTAGTACCGATTGCTCCAAAGACGCAAGTCGGAC  
ValThrProIleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGlu  
6301 ATGTAACACCAATAGACACTACCATCATGGCTAAGAACGGTTCTGCGTTAGCCTG  
TACATTGTGGTTATCTGTGATGGTAGTACCGATTGCTCCAAAGACGCAAGTCGGAC  
LysGlyGlyArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCys  
6361 AGAAGGGGGTCGTAAGCCAGCTCGTCATCGTGTCCCCTGGCGTGCCTG  
TCTTCCCCCAGCATTGGTCGAGCAGAGTAGCACAAGGGCTAGACCCGCACGCCACA  
GluLysMetAlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSer  
6421 GCGAAAAGATGGCTTGTACGACGTGGTTACAAAGCTCCCTGGCGTGTAGGGAAAGCT  
CGCTTTCTACCGAAACATGCTGCACCAATGTTCGAGGGAAACGGGACTACCCCTCGA  
TyrGlyPheGlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSer  
6481 CCTACGGATTCCAATACTCACCAGGACAGCAGGGTTGAATTCCCTCGTCAAGCGTGGAAAGT  
GGATGCTTAAGGTTATGAGTGGCTCTGTCGCCAACTTAAGGAGCACGTTCGCACCTTC  
LysLysThrProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGlu  
6541 CCAAGAAAACCCCAATGGGGTCTCGTATGATACCGCTGCTTGAACACTCCACAGTCACTG  
GGTTCTTGGGGTACCCCAAGAGCATACTATGGCGACGAAACTGAGGTGTCAGTGAC  
SerAspIleArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArg  
6601 AGAGCGACATCCGTACGGAGGGCAATCTACCAATGTTGTGACCTCGACCCCCAACGCC  
TCTCGCTGTAGGCATGCCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGG  
ValAlaIleLysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArg  
6661 GCGTGGCCATCAAGTCCCTCACCGAGAGGGCTTATGTTGGGGGCCCTCTACCAATTCAA  
CGCACCCGTAGTCAGGGAGTGGCTCTCCGAAATAACACCCCCGGGAGAATGGTTAAGTT  
GlyGluAsnCysGlyTyrArgArgCysArgAlaSerGlyValLeuThrSerCysGly  
6721 GGGGGGAGAACTGCGGCTATCGCAGGTGCCCGCGAGCGGGCGTACTGACAACACTAGCTGTG  
CCCCCCCTTGACGCCGATAGCGTCCACGGCGCGTCGCCGATGACTGTTGATCGACAC  
AsnThrLeuThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAsp  
6781 GTAACACCCCTACTGCTACATCAAGGCCGGCAGCTGTCGAGCCGAGGGCTCCAGG  
CATTGTGGGAGTGAACGATGTAGTCCGGGCCGTCGACAGCTGGCGTCCCAGG  
CysThrMetLeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGln  
6841 ACTGCACCATGCTCGTGTGGCGACGACTTAGTCGTATCTGTGAAAGCGCGGGGGTCC  
TGACGTGGTACGAGCACACACCCTGCTGAATCAGCAATAGACACTTCCGCCCCCAGG

FIG. 47-7

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63/63

6901	GluAspAlaAlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProPro AGGAGGACGCGCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCC TCCTCCTGCGCCGCTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGG
6961	GlyAspProProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnVal CTGGGGACCCCCCACAAACCAGAATACGACTTGGAGGCTCATACATCATGCTCCTCCA GACCCCTGGGGGGTGTGGTCTTATGCTAACCTCGAGTATTGTAGTACGAGGAGGTTGC
7021	SerValAlaHisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThr TGTCAGTCGCCACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCC ACAGTCAGCGGGTGCTGCCCGACCTTCTCCCAGATGATGGAGTGGGACTGGGATGTT
7081	ProLeuAlaArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGly CCCCCCTCGCGAGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCATT GGGGGGAGCGCTCTGACGCACCCCTCTGCGTTCTGTGAGGTCA GTTAAGGACCGATC
7141	AsnIleIleMetPheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePhe GCAACATAATCATGTTGCCCGACACTGTGGCGAGGATGATA CTGATGACCCATTCTCGTTATTAGTACAAACGGGGGTGTGACACCC CGTGTGAGGTAAAGA
7201	SerValLeuIleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAla TTAGCGTCCTTATAGCCAGGGACCAGCTGAA CAGGCCCTCGATTGCGAGATCTACGGGG AATCGCAGGAATATCGGTCCCTGGTCA ACTTGTCCGGGAGCTAACGCTCTAGATGCC
7261	CysTyrSerIleGluProLeuAspLeuProProIleIleGlnArgLeu CCTGCTACTCCATAGAACCACTTGATCTAC CTCCAATCTCAAAGACTC GGACGATGAGGTATCTGGTCA ACTAGATGGAGGTTAGTAAGTTCTGAG

FIG. 47-8

# INTERNATIONAL SEARCH REPORT

International Application No. PCT/US88/04125

## I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all).<sup>6</sup>

According to International Patent Classification (IPC) or to both National Classification and IPC  
 INT. Cl. (4) A61K 39/12; C12Q 1/70; C12N 15/00; C07K 7/10; A61K 37/04;  
 A61K 37/02; C07H 15/12  
 US Cl. 424/89; 435/5; 435/6; 435/172.2; 530/324; 530/350; 530/387; 536/27;

## II. FIELDS SEARCHED

Minimum Documentation Searched<sup>7</sup>

Classification System	Classification Symbols
U.S.	424/89; 435/5; 435/6; 435/172.2; 530/324; 530/350; 530/387; 536/27;

Documentation Searched other than Minimum Documentation  
to the Extent that such Documents are Included in the Fields Searched<sup>8</sup>

Online search conducted on chemical  
Abstracts and Biosis.

## III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup>

Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
PX	Journal of Virology, Volume 62 No.2 issued February 1988, Weiner et al "A single antigenomic open frame of the Hepatitis Delta virus encodes the epitope(s) of both Hepatitis Delta antigen polypeptides p 24 Delta and p 27 Delta". See pages 594-599.	1-17, 20-21 25, 27-28 40
X	Nature, Volume 323, issued 9 October 1986, Wang et al, "Structure, sequence and expression of the Hepatitis Delta viral genome". See pages 508-513	1-17, 20-21 25, 27 28, 40
A	Journal of Virological Methods, Volume 8 1984, Neurath et al "Strategies for detection of transfusion-transmitted viruses eluding identification by conventional serologic tests. II. Detection of host DNA in Human Plasmas with elevated alanine aminotransferase" See pages 73-85	22-24 29-31

- \* Special category of documents
- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

## IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
03 February 1989	03 APR 1989
International Searching Authority	Signature of Authorized Officer
ISA/US	Abdel A. Mohamed Abdel A. Mohamed

**III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)**

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
Y	U.S.A. 4,673,634, Seto et al, Published 16 June, 1987 (Column 1-10)	9-13, 20 22-24, 29-34
Y	U.S.A 4,702,909, Villarejos et al, Published 27 October, 1987 (column 1-10)	9-13, 18-20, 22-24 26, 29, 34, 39
Y	WO 82/00205, Coursgat et al, Published 21 January 1982 "Non-A Non-B Hepatitis Assay and Vaccine" (See the Whole Document)	22-34
Y	WO 87/05930, Foung et al, Published 8 October 1987 "Immortalized Virus-specific tissue cells" (See the whole Document)	35-37

**FURTHER INFORMATION CONTINUED FROM THE SECOND SHEET****V.  OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE<sup>1</sup>**

This international search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:

1.  Claim numbers \_\_\_\_\_, because they relate to subject matter<sup>1,2</sup> not required to be searched by this Authority, namely:

2.  Claim numbers \_\_\_\_\_, because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out<sup>1,2</sup>, specifically:

3.  Claim numbers \_\_\_\_\_, because they are dependent claims not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

**VI.  OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING<sup>2</sup>**

This International Searching Authority found multiple inventions in this international application as follows:

See Attached Sheet

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims of the international application. **Telephone Practice (See Attached Sheet)**

2.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims of the international application for which fees were paid, specifically claims:

3.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:

4.  As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

**Remark on Protest**

- The additional search fees were accompanied by applicant's protest.  
 No protest accompanied the payment of additional search fees.

PCT/US88/04125

ATTACHMENT TO FORM PCT/ISA/210, Part VI. 1

Telephone Approval:

\$280.00 payment is approved by the attorney Gladys H. Monroy on 3 February 1989 for Groups I,II and III; charge to Deposit Account No. 03-1952.

REASONS FOR HOLDING LACK OF UNITY IF INVENTION:

The invention as defined by Group II (claim 32) classified in class 424, subclass 89 and Group III (claim 40) classified in class 435, subclass 172.3, are drawn to a further alternative composition and a further alternative method additional to the compositions and methods of Group I and accordingly, lack of unity of invention under PCT Rule 13.2.

International Application No.: PCT/US68104125

Attachment to Form PCT/ISA/210, Part VI.

VI. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING:

I Claim 1-31 and 33-39, Drawn to purified HCV, poly-nucleotides thereof, Polypeptide therefore, recombinant vectors, hosts, Antibodies thereto and probes thereto; classified in classes 435, 536, 530 and 424; subclasses 235, 27, 300+ and 89+.

II Claim 32, Drawn to a polypeptide vaccine; classified in class 424, subclass 89.

III Claim 40, drawn to a method of isolating cDNA; classified in class 435, subclass 172.3.

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